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Title:
Perfect score:
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Maximum DB seq length: 200000000
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2: /SIDSZ/gcgdata/g
3: /SIDSZ/gcgdata/g
4: /SIDSZ/gcgdata/g
5: /SIDSZ/gcgdata/g
6: /SIDSZ/gcgdata/g
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000_DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
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10417.308 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
1	2151	100.0	2151	20	AAX86501	cDNA encoding a hu
N	2151	100.0	2151	21	AAA51229	Human beta-TrCP co
w	2151	100.0	2151	21	AAZ93350	Sequence encoding
4	2151	100.0	2151	21	AAZ93710	F -box protein hBe
ເກ	2151	100.0	2151	22	AAC84610	Human ZF11 protein
<u>Ф</u>	2120.8	98.6	3220	22	AAH90079	Human bone marrow
7	2114.8	98.3	2419	21	AAZ29233	Human cell signall
æ	2011.4	93.5	3622	22	ААН89966	Human bone marrow
S	2008.2	93.4	3003	22	AAK52699	Human polynucieoti

Probe #17692 used t	AA14/296 AA107701	22	370	9.7	208.4	44	0 0
#15003	AAI22005	2 2	370	9.7	208.4	. 43	O
bone marrow	AAK41254	22	370	9.7	208.4	42	a
	AAK15524	22	370	9.7	208.4	41	ი
Probe #12638 for g	ABA34172	22	370	9.7	208.4	40	ი
	ABA67080	22	370	9.7	208.4	39	O
•	ABA49167	22	370		•	38	o
	ABS02776	24	479	12.6	272	37	a
Probe #2737 used t	AAI02746	22	479	•	272	36	a
	AAI34184	22	479		272	35	O
tor g	AAI12828	22	479	12.6	272	34	C
3	AAK28263	22	479		272	3	O
Human brain expres	AAK02821	22	479	•	272	32	C
	ABA24312	22	479	12.6	272	31	O
-	ABA54530	22	479		272	30	a
	ABA44075	22	479		272	29	O
Drosophila melanog	ABL06080	23	9129		288	28	O
Human prostate exp	ABV58856	23	594		387.6	27	
cDNA encoding huma	ABK43155	23	951		435.4	26	
Beta-TRCP.N/SKP2.C	AAC84601	22	1561		518.8	25	
Differentiation In	AAZ09025	20	647		572.6	24	
	ABK86903	24	657		657	23	
Drosophila melanog	ABL06081	23	2387		676.4	22	
Human polynucleoti	AAI59364	22	4360	41.1	883.4	21	
Human polynucleoti	AAK52260	22	4344	41.1	883.4	20	
Human E3 ubiquitin	AAA51228	21	4230	-	883.4	19	
Human polynucleoti	AAI61150	22	2084	41.1	883.4	18	
Mouse ubiquitin li	AAA73131	21	1707	7	1443	17	
F-box protein FWD1	AAZ93714	21	2175	8	1682.2	16	
Human polynucleoti	AAK51716	22	2207	ω.	389	15	
Human polynucleoti	AAK51717	22	2366	78.9	1697.8	14	
Human polynucleoti	AAK51715	22	2285	æ	697	13	
Human beta-transdu	AAA73132	21	1707	9	17	12	
Human polynucleoti	AAK52701	22	3003	93.4		11	
Human polynucleoti	AAK52700	22	3003	93.4	2008.2	10	

ALIGNMENTS

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RESULT 1
AAX86501
ID AAX8
                                                          AAX86501 standard; cDNA; 2151 BP.
30-SEP-1999 (first entry)
                             AAX86501;
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Beta-transducin repeat containing protein; beta-TrcP; Skplp; proteosome degradation pathway; Vpu protein; beta-catenin; human immune deficiency virus-1; HIV-1; cellular protein; IKappaB; ubiquitinylation; phosphorylated protein; tumour; apoptosis; Alzheimer's; antiviral; antitumour; cell cycle regulation; protein degradation; and anti-inflammatory; osteo-articular inflammation; acute inflammation; tumour necrosis factor; ss.

Homo sapiens.

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XX	o X	PD	XX	ΡN	XX	ΤŦ	Ę	FΤ	FΤ	FΗ	X	SO	XX	X	X	XX	W	X	KW.	XΨ	XX	DE
20 OFM +000	29-TAN-1999.	05-AUG-1999.		WO9938969-A1.					CDS	Key		Homo sapiens.		tumour necrosis factor; ss.	and anti-inflam	antiviral; anti	ubiquitinylatio	human immune de	proteosome degi	Beta-transducir		cDNA encoding a
	99WO-FR00196					<pre>/note= "beta-transducin repeat containing protein"</pre>	/product= beta-TrcP	/*tag= a	701779	Location/Qualifiers				s factor; ss.	and anti-inflammatory; osteo-articular inflammation; acute inflamma	antiviral; antitumour; cell cycle regulation; protein degradation;	ubiquitinylation; phosphorylated protein; tumour; apoptosis; Alzhei	human immune deficiency virus-1; HIV-1; cellular protein; ikappas;	proteosome degradation pathway; Vpu protein; beta-catenin;	Beta-transducin repeat containing protein; beta-TrcP; Skpip;		cDNA encoding a human beta-transducin repeat containing protein.

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The present sequence encodes a human beta-transducin repeat containing protein (beta-TrcP). The protein directs proteins to the proteosome degradation pathways. The protein is able to interact with the Vpu protein of human immune deficiency virus-1 (HIV-1), cellular proteins CC IkappaB or beta-catenin (bC) and/or protein Skpip. The protein controls CC ubiquitinylation of phosphorylated proteins and thus their targeting to proteosomes for degradation. Depending on whether the process is CC inhibited or promoted, the result may be delayed breakdown of CD4 (in CC cases of HIV-1 infection); increased activity of IkB (and thus reduced activity of NrkappaB) and increased activity of mutant bc in tumour CC cells, or increased bc survival (and reduced apoptosis) in Alzheimer's CC patients. The beta-TrcP protein, and its active peptide fragments, or its could call, are used to screen for anti HIV-1 agents (antivirals), CC degradation in human tumour cells, and anti-inflammatory agents that disrupt activation by NrkappaB. Fragments of the protein are also CC useful for treating osteo-articular inflammatory or cute inflammation or accute inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 2151;
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Best Local (
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30-JAN-1998;
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                 GAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCGTATCTTAAA
                                                       AAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTGGAATTTGTG
                                                                                          AAGGAACTGTGTGAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTGGAATTTGTG
                                                                                                                                GGCACTTCCAGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTATGAAAAGGAA
                                                                                                                                                   GGCACTTCCAGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTATGAAAAGGAA 360
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TCCTCAGAGAGAGAAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATACCAGAGAAG
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TTTGATAACAAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTGTGGGATCTT
                              TTTGATAACAAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTGTGGGATCTT
                                                              GAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTCGA
                                                                                GAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTCGA
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                                                                                                                                                                                                                                                  Human beta-TrCP coding sequence
                                                                                                                                                                                                                                                                                                                       AAA51229 standard;
                                                                                                     WO200034447-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 2151;
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Best Local Similarity
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03-FEB-1999;
15-MAR-1999;
WPI; 200
P-PSDB;
                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                               F-box protein; FBP; diagnosis; treatment; screening; agonist; antagonist; proliferative disorder; differentiative disorder; breast cancer; prostate cancer; ovarian cancer; cancer; small cell lung carcinoma; immune disorder; cardiovascular disorder;
                                   Chiaur DS,
                                                                                                                                27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                             Sequence encoding F-box protein FBP-1.
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                                                                                                                                                                                                                                                                                         inflammatory disorder; human; ss.
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                                 Pagano M,
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99US-0124449
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Query Match
Best Local Similarity
Matches 2151; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FBP gene expression. Cells expressing such proteins or their fragments are useful for account.
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useful in diagnosis of the disorders.
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                                                                                     Targeting degradation of polypeptide useful for treating cancer and other proliferative disorders, involves conjugating polypeptide with ubiquitin protein ligase or inhibiting ubiquitination using organic
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The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin ligases) which can be used for the targetted degradation of a target polypeptide in vivo. Targetted degradation is achieved by expressing the ubiquitin ligase in a cell linked to the interaction domain of

Claim 10; Page 171; 185pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the target polypeptide and thereby recruiting the target polypeptide to the ubiquitin ligase. Such methods are useful for decreasing or increasing the level of a target polypeptide and for creating and expressing a destabilized polypeptide which is subjected to SCF useful for preventing or treating diseases caused by the presence of abnormal amount of the specific polypeptides, for drug discovery and for gene therapy. Diseases treated include cancer, by degradation of microbial infections. The method provides a quick and easy alternative to gene knockout technology. The target polypeptide can be degraded at all stages, or a specific stage, of development in the method at all stages, or a specific stage, of development in the
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1 TGCGTTGGCTGCGGCCTGGCACCAAAGGGGCCGCCCCGGCGGAGAGCGGACCCAGTGGCC

Query Match Best Local Sim Matches 2151;

Similarity

100

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Score 2151; Pred. No. 0;

DB

Conservative

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Mismatches

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Sequence 2151 BP; 628 A; 467 C; 513 G; 543 T; 0 other;

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                                     The invention relates to methods of altering the polypeptide levels in a cell, using proteins selected from S-phase kinase associated proteins 1 and 2 (SKP1, SKP2), SKP2-like proteins (2F) and CUI-1 (a member of the cullin/CDC53 family of proteins). The method is useful for altering the level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bc1-2 polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for detecting tumours, and in monitoring tumor treatment in a mammal. Agents that modulate interactions between SKP and target proteins are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2101
                                                                                                                                                                                                             Modulating polypeptide levels in a cell, diagnosing and treating involves altering levels of proteins such as S-phase kinase associated proteins 1, 2 and cullin/CDC53 proteins -
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P-PSDB; AAB48298.
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                             treating tumours.
                                                                                                                                                                                Examples; Page 129-130; 162pp; English.
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1080 1080	AGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGATGTAAATACAGGT	1021 1021	Ωу
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960	CAGAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGGGATAAAAACACATTG	901 901	Оу
900	CAGAGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGTTTACAGTATGATGAT 	841 841	Фр
840 840	AJAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGTGGAAGACATAGTTTA	781 781	Qу
780 780	AAAAACAAACCTCCTGACGGGAATGCTCCTCCCAACTCTTTTTATAGAGCACTTTATCCT	NN	Дb
720 720	AGGACAGATTCTCTGTGGAGAGGCCTGGCAGAACGAAGAGGATGGGGACAGTATTTATT	661 661	DЬ
660	GAATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAGAGAATGGTC	0 0	Db Qy
600	GAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTTGTGTGCAAG	541 541	Db 04
540 540	CCTATGTTGCAGAGAGTTTCATAACTGCTCTGCCAGCTCGGGGATTGGATCATATCGCT	481 481	Db Qy
48 0 48 0	GAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCGTATCTTAAA	421 421	ДУ
420 420	AAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTGGAATTTGTG	361 361	Db Qy
360 360	GGCACTTCCAGTATGATTGTGCCCAAGCAACCGAAACTCTCAGCAAGCTATGAAAAGGAA	301 301	ДУ ДБ
300	TGTTTAGCAAGCACTGCTATGAAGACTGAGAATTGTGTGGCCAAAACAAAC	241 241	Дb
240 240	AATTCACTTAGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGTA	181 181	ОУ
180 180	TCCTCAGAGAGAGAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATACCAGAGAGAG	121 121	Qy Db
120 120	TCGGCGATTATGGACCCGGCCGAGGCGGTGCTGCAAGAGAAGGCACTCAAGTTTATGAAT	61	Qy Db
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                  immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIY), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. hamophilla), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence
                                                                                                                                                                                                                                                                                                                                                                       The present sequence is one of 251 novel human polynucleotides expressed in the bone marrow. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various transports.
                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is one of 251 novel expressed in the bone marrow. The noturn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; bone marrow; antiinflammatory; cytostatic; neuroprotec antiviral; antibacterial; antifitingal; anti-HIV; haemostatic; immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; c
                                                                                                                                                                              Sequence
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14-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders -
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၁QA,
                                                                                                                                                                                                                       istem disorder such as Alzheimer's disease. Detection of the presence increased expression of the polynucleotide or the protein it codes is useful for the diagnosis and/or prognosis of one more types of cancer. The polynucleotide and polypeptide can be ed as nutritional sources or supplements and in the screening of
                                                                                                                                                Match
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                                                                        TGCGTTGGCTGCGGCCTGGCACAAAGGGGGGGCCCCGGCGGAGAGCGGACCCAGTGGCC
                             2001-488707/53.
TGCGTTGGCTGCCTGGCACCAAAGGGGCGGCCCCGGCGGAGAGAGCGGACCCAGTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bone marrow cDNA, SEQ ID NO: 323.
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                                                                                                                                                                                                            compounds as potential drugs.
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2000US-062312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0250583.
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2000US-0552317.
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Pred. No. 0;
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u C, Xue AJ, Yang
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Yang Y, Zhang J;
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                                                                                                                                                                                                                                                                                                                                             Matches 2119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a cDNA obtained from Incyte clone 3239149 of COLAUCTOI library. It encodes cell signalling protein 12 (CSIGP-12). It is expressed in musculo-skeletal, gastrointesinal and nervous tissues. Fragments of CSIGP encoding nucleic acid can be used as hybridisation probe for detecting CSIGP related sequences or allelic variants. Recombinant CSIGP can be produced in host cells by transforming them with genetically engineered vectors. Agonists or antagonists can be used in the treatment of cell proliferative and inflammatory disorders associated with decreased or increased CSIGP expression. CSIGP is used in the diagnosis, prevention and treatment of cell proliferative disorders like arteriosclerosis, cirrhosis, cancer hepatitis and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2419 BP; 671 A; 531 C; 625 G; 590 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders like AIDS, Addison's disease, multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Page 87-88; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cell signaling proteins useful for, e.g. diagnosing proliferative and inflammatory disorders
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/product= "Cell Signalling Protein-12"
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                                                                                                                                        bone marrow cDNA,
                                                             immunodeficiency virus; HIV; autoimmune
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19-OCT-2000;
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25-APR-2000;
09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is one of 251 novel human polynucleotides expressed in the bone marrow. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one used as nutritional sources or supplements and in the screening of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ford
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; 2000US-0598042.
; 2000US-0620312.
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Werhman T, Xu
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u C, Xue AJ, Yano
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of carcon labels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT,
Zhao QA,
Xue AJ,
Sequence 3003 BP; 807 A; 703 C; 721 G; 772 T; 0 other;
                                      Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy - \,
                                                                                                          treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                      inflammation.
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Wang J, Zhang J, Ren F, Chen
Wejhrman T, Goodrich R;
                                                    the relevant pages from the sequence listing
                                                                        2111 (AAK52582) and 3666
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Chen R, Wang
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                                           TGTATTCGATTTGATAACAAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTG
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                                                                                               AGTTCACATGATGACACAATCCTCATCTGGGACTTCCTAAATGATCCAGCTGCCCAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                       vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                              Tang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy;
                                             Claim 1; Page 4585-4586;
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30-NOV-2000;
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                                                                            Nucleic acids encoding polypeptides with cytokine-like activities
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DB; AAM79567.
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Yang Y, Wejhrman
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2000US-0598075
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                      GTGTGCAAGGAATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAG
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                                                                                                      CATAGTTTACAGAGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGTTTACAG
                                                                                                                                                                                                                                                                                                                                            AGAATGGTCAGGACAGATTCTCTGTGGAGAGGCCTGGCAGAACGAAGAGGATGGGGACAG
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                                                                                    CATAGTTTACAGAGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGTTTACAG
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2030 2217	11 ACTCAGCACAACTGACTGCTTCAGTGCTGCTATCAGAAGATGTCTTCTATCAATTGTGAA	Qy 197 Db 215	
1970 2157	1 AGCAGGGCTTTGAGACTCCTGTTGGGACACAGTTGGTCTGCAGTCGGCCCAGGACGGTCT	Qу 191 Db 209	
1910 2097	31 CAGGATGAGCAACAACAGTAACAATCAAACTACTGCCCAGTTTCCCTGGACTAGCCGAGG 		
1850 2037)2 TGACCTCATACTTGCCCAGGACCCATTAAAG-TTGCGGTATTTAACGTATCTGCCAATAC 	Qy 179 Db 197	
1791 1977	32 GAACCCCCCGTTCCCCTTCTCGAACATACACCTACATCTCCAGATAAATAA	Qy 173 Db 191	
1731 1917	2 AGTTCACATGATGACACAATCCTCATCTGGGACTTCCTAAATGATCCAGCTGCCCAAGCT	р р	
1671 1857	2 CTTGTGGAGCATTCCGGAAGAGTTTTTCGACTACAGTTTGATGAATTCCAGATTGTCAGT	Qy 161 Db 179	
1611 1797	2 TGGGATCTTGTGGCTGCTTTGGACCCCCGTGCTCCTGCAGGGACACTCTGTCTACGGACC	Qy 155 Db 173	
1551 1737)2 TGTATTCGATTTGATAACAAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTG 	Qy 149 Db 167	
1491 1677	2 TGGGACATAGAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGT 	Qy 143 Db 161	
1431 1617	72 TGTTTGCAGTACAGGGACAGGCTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTA 	Qy 137 Db 155	
1371 1557	2 TGGAACACAAGTACTTGTGAATTTGTAAGGACCTTAAATGGACACAAACGAGGCATTGCC 		
1311 1497	52 GTTGTAGACTTTGATGACAAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTA 	₽ ₹	
1251 1437)2 GCCTCCCAACTGACATTACCCTCCGGAGGGTGCTGGTCGGACACCGAGCTGCTGTCAAT	Qy 119 Db 137	
1191 1377	22 TTCAATAATGGCATGATGGTGACCTGCTCCAAAGATCGTTCCATTGCTGTATGGGATATG	Qy 113 Db 131	
1131 1317	2 AATACAGGTGAAATGCTAAACACGTTGATTCACCATTGTGAAGCAGTTCTGCACTTGCGT	Qy 107 Db 125	
1071 1257	.2 TATGATGAGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGATGTA	Оу 101 Db 119	
1011 1197	2 AACACATTGGAATGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCCTCTGTCTCCAG	Qy 95 Db 113	

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RESULT 11
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27-APR-2000; 2000US-0560875.

20-JUN-2000; 2000US-0598075.

19-JUL-2000; 2000US-0620325.

01-SEP-2000; 2000US-0654936.

15-SEP-2000; 2000US-0663561.

20-OCT-2000; 2000US-0693325.

30-NOV-2000; 2000US-0728422.
                                                                                                                                                                                   The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating
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                                                              Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                    activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                             Claim 1; Page 4586-4587; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-476283/51.
P-PSDB; AAM79568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen Xue AJ, Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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                                                                                                                      inflammation
                                                                                                                                    treatment of cancer, leukaemia, nervous system disorders, arthritis and
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   93.4%;
 Score 2008.2;
DB 22; Length 3003;
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R, Wang ZW;
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                  CCATTGGTTCCAGACAAGGTGACTTATAAATATATTTAGTGTTTTGCCAGAA 2143
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                                                                 TGATTGGAACTTTTAAACCTCCCCTCCTCCTCCTTTCACCTCTGGCACCTAGTTTTTC
                                                                                                                   ACTCAGCACAACTGACTGCTTCAGTGCTGCTATCAGAAGATGTGTTCTATCAATTGTGAA
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CCATTGGTTCCAGACAAAGGTGACTTATAAATATATTTAGTGTTTTGCCAGAA 2330
                                                   TGATTGGAACTTTTAAACCTCCCCTCCTCCTCCTTTCACCTCTGCACCTAGTTTTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes an F-box motif protein of ubiquitin ligase SCF complex which promotes the ubiquitination of IkappaB or beta-catenin and is constituted by Skpl protein, Cull protein and a complex (SCF complex) of F-box protein containing F-box motif and WD40 repeat motif and has the amino acid sequence of 45 residues (AAB12811) or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin ligase FWD1 protein) and (AAB12813, which is human beta-transducin repeat containing protein (beta-TrCP)). The F-box protein can be used to the gene therapy of colon cancer by being recombined to a virus vector. The present sequence encodes the human beta-TrCP protein from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ubiquitin ligase SCF complex; F-box protein; ubiquitination; IkappaB; beta-catenin; Skpl; Cull; F-box motif; WD40 repeat motif; FWD1; gene therapy; colon cancer; beta-transducin repeat containing protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1707 BP; 514 A; 349 C; 414 G; 430 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 17; 19pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F-box protein of ubiquitin ligase SCF complex which promotes the ubiquitination of IkappaB or beta-catenin
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                                                                                                                                                                                                                                                                                                                                              70 ATGGACCCGGCCGAGGCGGTGCTGCAAGAGAGAGCACTCAAGTTTATGAATTCCTCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                        AGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGTATGTTTAGCA
                          AGCACTGCTATGAAGACTGAGAATTGTGTGGGCCAAAACAAAACTTGCCAATGGCACTTCC
                                                                                                                                                                                                                                                                                      AGAGAAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATACCAGAGAAGAATTCACTT 189
ATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCGTATCTTAAACCTATGTTG
                                              TGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAAGTGGAATTTGTGGAACATCTT
                                                                                     AGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTATGAAAAAGGAAAAGGAACTG
                                                                                                                                                AGCACTGCTATGAAGACTGAGAATTGTGTGGCCAAAACAAAACTTGCCAATGGCACTTCC
                                                                                                                                                                                                                                                                     AGAGAAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATACCAGAGAAGAATTCACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention.
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                                                                                                                                                                                                                                                                                                                                                                                                        79.48;
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Pred. No. 0;
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                                       AAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTGTGGGATCTTGTGGCTGCT 1569
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27-APR-2000; 2000US-0560875.

20-JUN-2000; 2000US-0598075.

19-JUL-2000; 2000US-0629325.

01-SEP-2000; 2000US-0654936.

15-SEP-2000; 2000US-0663561.

20-CCT-2000; 2000US-0693325.

30-NOV-2000; 2000US-0728422.
                                                                                                                                                                                                                                                                                                                       Tang YT,
Zhao QA,
Xue AJ,
The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78333-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy;
vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
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                                                                                                                                                                                Claim 1; Page 1177-1180; 6221pp; English.
                                                                                                                                                                                                                 Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                       P-PSDB; AAM78582
                                                                                                                                                                                                                                                                                          WPI; 2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nervous system disorder; arthritis; inflammation; ss
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                                                                                                                                                                                                                                                                                                                       Yang Y, Wejhrman T,
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                                                                                               TATGATGATCAGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGGGATAAA 951
                                                                                                                                       CATAGTTTACAGAGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGTTTACAG
                                                                                                                                                                                                                CTTTATCCTAAAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGTGGAAGA 831
                                                                                                                                                                                                                                                                      TATTTATTCAAAAACAAACCTCCTGACGGGAATGCTCCTCCCAACTCTTTTTATAGAGCA
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TATGATGAGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGATGTA 107:
                          AACACATTGGAATGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCCTCTGTCTCCCAG
                                                     AACACATTGGAATGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCCTCTGTCTCCAG 1011
                                                                                  TATGATGATCAGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGGGATAAA 1116
                                                                                                                                                                   CATAGTTTACAGAGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGTTTACAG
                                                                                                                                                                                               CTTTATCCTAAAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGTGGAAGA
                                                                                                                                                                                                                                                      TATTTATTCAAAAACCAAACCTCCTGACGGGAATGCTCCTCCCAACTCTTTTTATAGAGCA
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                                                                                                                                                         Similarity
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TGACCTCATACTTGCCCAGGTATCGAAATCGATTATGTACATAAC
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RESULT 14
AAK51717
AAK51717 standard;
cDNA; 2366
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ВP

Human polynucleotide SEQ ID 06-NOV-2001 (first entry)

NO 262

Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss. Homo sapiens gene therapy;

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Best Local
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19-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment of cancer, leukaemia, nervous system disorders, arthritis and
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20-OCT-2000;
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DB; AAM78584.
                                            GAATTTGTGGAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCG
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GAATTTGTGGAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCG
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                                                                   TGTATTCGATTTGATAACAAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTG 1551
                                                                                                                     TGGGACATAGAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGT
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities,
                                                                   Claim 1; Page 1180-1183; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                    Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                  Nucleic acids encoding
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27-APR-2000;
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                                                                                                                                                                                                  Sequence 2207 BP; 615 A; 478 C; 555 G; 559
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TCTAATTGGAGATGTGGAAGACATAGTTTACAGAGAATTCACTGCCGAAGTGAAACAAGC
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1918 CATAAC 1923
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                                                                                                                                           AATGATCCAGCTGCCCAAGCTGAACCCCCCCGTTCCCCTTCTCGAACATACACCTACATC 1770
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                                                           TCCAGATAAATAACCATACACTGACCTCATACTTGCCCCAGGTATCGAAATCGATTATGTA 1917
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Search completed: February 21, 2003, 22:17:15 Job time : 484 secs

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Result
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Mi26	78543 UI- 14360 C08	BQ340149 QV2-NN200 BM211073 C0800D04-	1d93	BE284066 601099246	AV71	BQZ11349 U1-K-U11- AA478504 ZW95b10.r	UI-R	011d(C0845E1	вл048898 вл048898	L642623	AGENCON	KFZp686A	BF781002 602106631	60285273	ux60f06.	L556068	BF076123 225612 MA	ur63q08	naf16h04	DT-M-FTO	BM9443U4 UI-M-EHUD	60317397)KFZp43	60288932	G518761 602	G722472 602	29037 602	Q948186 AGE	11822845 60304	7 60118635

ALIGNMENTS

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source	FEATURES											COMMENT	JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	BE782628
1709	Location/Qualifiers	High quality sequence stop: 655.	Plate: LLAM9617 row: f column: 13	http://image.llnl.gov	found through the I.M.A.G.E. Consortium/LLNL at:	Clone distribution: MGC clone distribution information can be	DNA Sequencing by: Incyte Genomics, Inc.	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	cDNA Library Preparation: Life Technologies, Inc.	Tissue Procurement: ATCC	Email: cgapbs-r@mail.nih.gov	Contact: Robert Strausberg, Ph.D.	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	NIH-MGC http://mgc.nci.nih.gov/.	1 (bases 1 to 709)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human .	EST.	BE782628.1 GI:10203826	BE782628	mRNA sequence.	601465751F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868812 5',	BE782628 709 bp mRNA linear EST 20-OCT-2000	

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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                   AGTGGCCAGTTTCCCTGGACTAACCGAGGAGCCAGCGTTGGAGACTCCTGTGG
                                                                                                                                                                                                                                                                                                                                    GTTGCGGTA-TTAACGTATCTGCCAATACCAGGATGAGCAACAACAGTAACAATC-AACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCTACATCTCCAGATAAATAACCATACACTGACCTCATACTTGCCCAGGACCCCATTAAA 598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCTTAAATGGACACAAACGAGGCATTGCCTGTTTGCAGTACAGGGACAGGCTGGTAGTG 179
                                                                          UI-M-EX0-bxj-1-06-0-UI.rl NIH_BMAP_EX0 Mus musculus cDNA clone
                             BQ444188
                                                                                                        BQ444188
  BQ444188.1 GI:21247300
                                                     IMAGE: 5709077 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 a
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/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
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/db_xref="taxon:9606"
/clone="IMAGE:3868812"
/clone_lib="NIH_MGC_67"
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Pred. No. 7.5
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GATTTCATAACTGCTCTGCCAGCTCGGGGATTGGATCATATCGCTGAGAACATTCTGTCA 555
                                                                                                                                                                                                                                                                                                                                                          AAGTATTTTGAGCAGTGGTCAGAGTCTGATCAAGTGGAATTTGTAGAACACCTTATATCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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//lab_bost="whole brain;
/dev_stage="embryo 15.5 dpc"
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//note="Organ: brain; vector: pyx-asc; Site_1: Book I;
//note="Organ: brain; vector: pyx-asc; Vector:
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/db_xref="taxon:10090"
/clone="IMAGE:5709077"
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKFZp434M1528_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434M1528 5', mRNA sequence.
                                                                                                                                           Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
                                                                                                                                                            Please contact the RZPD:
                                                                                                                                                                      This clone (DKFZp434M1528) is available at the RZPD in
                                                                                                                                                                                       No s1 sequence available
                                                                                                                                                                                                      German Genome Project
                                                                                                                                                                                                               Braunschweig/Germany) within the cDNA sequencing
                                                                                                                                                                                                                                                                                                                      Contact: Bloecker H
                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                       Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 652)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                      Klopferspitz 18a D-82152 Martinsried, Germany
                                                                                                                                                                                                                                                                                                                                                 (Bloecker, et al.)
                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp434M1528"
/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
                                                                                                                             Location/Qualifiers
   /note="Vector:
                  /lab_host="DH10B"
pSport1; Site_1: NotI;
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Site_2:
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5', mRNA sequence.
BQ425358
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Mammalia; Eutheria; Primates; C:
1 (bases 1 to 851)
NIH-MGC http://mgc.nci.nih.gov/
                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                EST
                                                                      Contact: Robert Strausberg, Ph.D
                                                                                         Unpublished (1999)
                                                                                                      National Institutes of Health, Mammalian
                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                              BQ425358.1
cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                     GTATTTATTCAAAAACAAACCTCCTGACGGGAATGCTCCTCCCAA 755
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                                                                                                                                GTATTTATTCAAAAACCAAACCTCCTGACGGGAATGCTCCTCCCCA 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATATTGCTGAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTT 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATATCGCTGAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTT
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                                                                                                                                                                                                                                                                                               AGAATGGTCAGGACAGATTCTCTGTGGAGAGGCCTGGCAGAACGAAGAGGATGGGG-ACA 710
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BM465280
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/tissue_type="retinoblastoma"
/lab_host="DH108 (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.75 kb. Library constructed by Lif
Technologies."
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                                                                                                                                                                                         TIGGAAIGCAAGCGAATICTCACAGGCCAIACAGGTTCAGICCTCTGTCTCCCAGIAIGAT 1017
                                                                      GAGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGATGTAAATACA 439
                                                                                                                     GAGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGATGTAAATACA 1077
                                                                                                                                                                TTGGAATGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCCTCTGTCTCCAGTATGAT
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AGENCOURT_6427660 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:55020755', mRNA sequence.
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 973)
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Plate: LLAM12139 row: k column: 04
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo
Average insert size 1.75 kb. Library constructed by
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Best Local Similarity
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 662
                                                                    602 AATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAGAGAATGGTCA 661
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 AATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAGAGAATGGTCA 60
                                                                                                      649;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 758)
                                                                                                                                                                                           212
                                                                                                                                                                                  /Clone_lib="NIH_MGC_17"
/Clone_lib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
/lab_host="DHIOB (phage_resistant)"
/lab_host="DHIOB (phage_resistant)"
/note="Organ; muscle; Vector: pOTB9; Site_1: EcoRI;
/note="Organ; muscle; Vector: pOTB9; Sites using the Directionally cloned into EcoRI/MoI sites using the Directionally cloned into EcoRI/MoI Sites using the following 5' adaptor: GGCAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
12 a 149 c 202 g 195 t
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE: 3530341"
                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                   28.5%;
                                                                                                      0
                                                                                                                   Score 613.2; DB 10
Pred. No. 1.4e-172;
                                                                                                        Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        758 bp
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                                                                                                        Indels
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AUTHORS
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                                       FEATURES
                                                                                                                                                                                                               COMMENT
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     /organism="Homo sapiens"
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1260 CTTTGATGACAAGT 1273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGGATGT-AAATACAGGT 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTGACATTACCCTCCGGAGGGTGCTGGTC-GGACACCGAGCTGCTGTCAATGTTGTAGA 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCATGATGGTGACCTGCTCCAAAGATCGTTCCATTGCTGTATGGGATATGGCCTCCCCA 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAATGCTAAACACGTTGATTCACCATTGTGAAGCAGTTCTGCACTTGCGTTTCAATAAT 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGGGATAAAAACACATTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGACATTACCCTCCGGAGGGTGCTGGTCGGGACCACGAGGCTGCTGTCATGTTGTTGA 660
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                                                                                                                                                                                               Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      601186356F1 NIH_MGC_8 Homo sapiens
                                                                           DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM239 row: o column: 14
                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                  High quality sequence stop: 610
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                      Location/Qualifiers
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RESULT 8
BI822845
           DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 AAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGTGGAAGACATAGTTTAC
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                                  BI822845
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/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site_1: xhoI; Site_2: forer: potB7; coned into EcoRI/XhoI sites using the following 5; calaptor: GCACCAG(G) Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
02 a 134 c 179 g 177 t
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97.7%;
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Pred. No. 2.8
                           828 bp
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2.8e-171;
ches 12; Indels 3;
                           mRNA
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                    EST 04-OCT-2001
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AUTHORS
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472 TATCTTAAACCTATGTTGCAGAGAGATTTCATAACTGCTCTGCCAGCTCGGGGATTGGAT 531
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                                                      488 GAATTTGTGGAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCG
                                                                                   412 GAATTTGTGGAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCG 471
                                                                                                                                                                 428 GAAAAGGAAAAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTG
                                                                                                                                                                                                                    352 GAAAAGGAAAAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTG
                                                                                                                                                                                                                                                                           368 CTTGCCAATGGCACTTCCAGTATGATTGTGCCCAAGCAACCGAAACTCTCAGCAAGCTAT 427
                                                                                                                                                                                                                                                                                                           292 CTTGCCAATGGCACTTCCAGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                  232 GAAACAGTATGTTTAGCAAGCACTGCTATGAAGACTGAGAATTGTGTGGGCCAAAACAAAA 291
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11451 row: h column: 18
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="DHIOB"
/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, site_1: ECORV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (ECORV site is
destroyed upon cloning). Average insert size 18 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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/clone_lib="NIH_MGC_115"
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                                                                                      TTCCAGAATTCCTCAGAGAGAGAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATA 209
                                                                                                         TTTATGAATTCCTCAGAGAGAGAGAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATA 171
                                                                                                                                                  606;
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1 (bases 1 to 1147)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: ATCC
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AGENCOURT_8878641 NIH_MGC_71
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Plate: LLAM13986 row: a column: 24
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                           324
                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                      /tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb.
a 289 c 284 g 250 t
                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6464639"
                                                                                                                                                                                                                                                                                                              /clone_lib="NIH_MGC_71"
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97.6%;
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Pred. No. 1.7e-164;
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                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                           National Institutes of Health, Mammalian Unpublished (1999)
                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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                                                                                                  /organism="Homo sapiens"
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GAGAATGGTCAGGACAGATTCTCTGTGGAGAGGGCCTGGCAGAACGAAGAGGATGGGGACA 710
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http://image.llnl.gov
Plate: LLCM1808 row: o column: 16
High quality sequence stop: 703.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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/db_xref="taxon:9606"
/clone="IMAGE:4906215"
/clone_1ib="NIH_MGC_17"
/clsue_1ib="nrhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pOTB7; Si
Site_2: XhoI; cDNA made by oligo-dT pri
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                                  Site_1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGTCAGAGTCAAGTGGAATTTGTGGAACATCTTATATCCCAAATGTGTCATTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               637;
                                              mRNA sequence. BG722472
BG722472.1 GI:14001659
EST.
                  Homo sapiens
                                                                                                     BG722472
602693716F1 NIH_MGC_97
    Eukaryota;
                                 human.
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                    Homo sapiens cDNA clone IMAGE: 4825970
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                                                                                                                      linear
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594 GTGCAAGGAATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAGAG 653
                                                                         534 TATCGCTGAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGCTGAACTTGT 593
                                                                                                                                           521 CTTAAACCTATGTTGCAGAGAGATTTCATAACTTGCTCTGCCAGCTCGGGGATTGGATCA 580
                                                                                                                                                                                    475 CTTAAACCTATGTTGCAGAGAGATTTCATAAC-TGCTCTGCCAGCTCGGGGATTGGATCA 533
                                                                                                                                                                                                                                                                                           415
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                                                                                                                                                                                                                                                                                                                                                                                                                            341 GCCAATGGCACTTCCAGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTATGAA
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                                                                                                                                                                                                                                       461 TTTGTGGAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCGTAT
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                                                TATTGCTGAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTTGT 640
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                                                                                                                                                                                                                                                                                                                                                                           AAGGAAAAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTGGAA 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 752)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: LLAM10739 row: p column: High quality sequence stop: 728.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-X-MoI (gtoga); Oligo-df primed using primer 5:-TTTTTTTTTTTTTVN-3; size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NIGRI, National Institutes of Health). Note: this is a NIH_MGC Library." a 143 c 194 g 177 t
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/clone="IMAGE:4825970"
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98.8%;
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Pred. No. 1.6e-158;
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                                                                                                            CACTTAGACAGACTTACAACAGCTGTGCCAGGCTTTGCATAAACCAAGAGACACTATGTC 180
                                                                                                                                CACTTAGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGTATGTT 244
                                                                                                                                                                                    CAGAGAGAAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATACCAGAGAAGAATT 120
                                    TAACAAGCACTGCTATGAAGACTGAAAATTGTGTGGCCAAAGCCAAACTTGCCAATGGCA
                                                                       TAGCAAGCACTGCTATGAAGACTGAGAATTGTGTGGCCAAAACAAAACTTGCCAATGGCA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 789)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Plate: LLAM8536 row: k column:
High quality sequence stop: 587.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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BG518761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 257
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo of Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

a 176 c 202 g 154 t
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/clone="IMAGE:3491843"
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/strain="CZECH II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="spontaneous tumor, metastatic to mammary.
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86.1%;
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Pred. No. 7e+149; 
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                                                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11122 row: i column: 05
                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                    National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
1 (bases 1 to 637)
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                                                                                                                                                                                           quality sequence stop:
/db_xref="taxon:10090"
/clone="IMAGE:5044684"
/clone_lib="NCI_CGAP_Kid14"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B_(T1_phage=resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                               /organism="Mus musculus"
/strain="FVB/N"
                                                                                                                                                                        Cocation/Qualifiers
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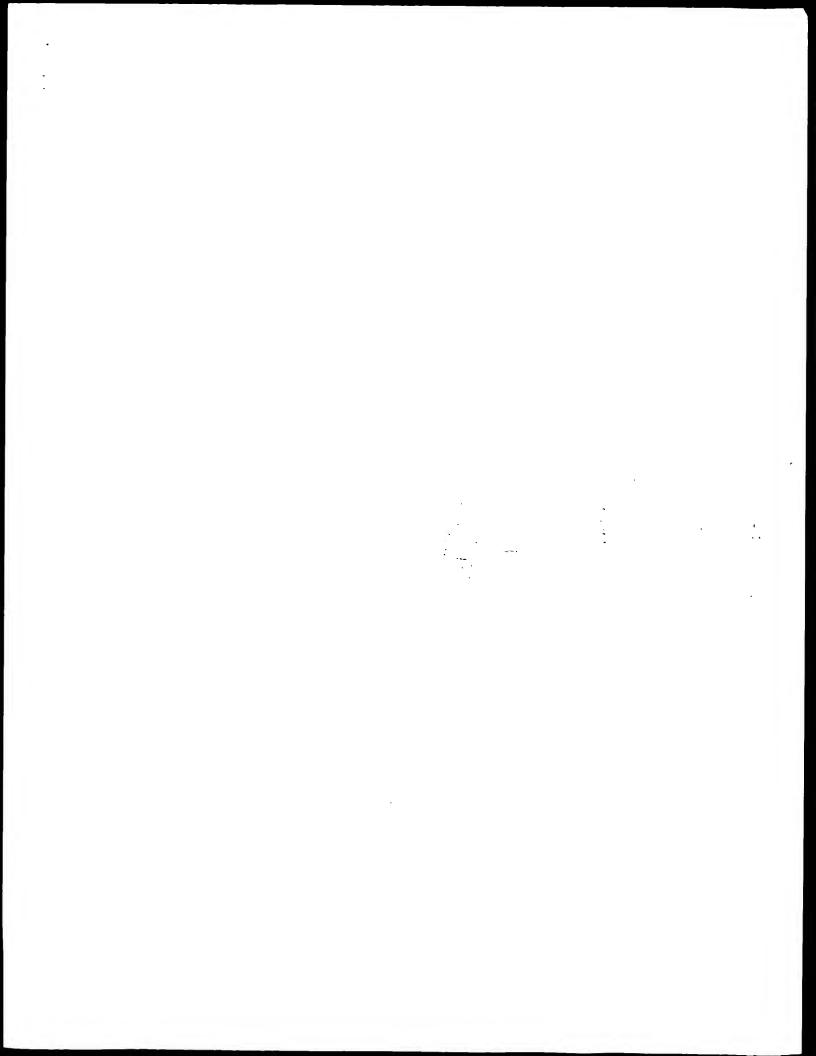
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                                                                                                                                                                                         DKFZP434D2317_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZP434D2317 3', mRNA sequence.
Contact: Bloecker H
               Unpublished (1999)
                                                         Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Gassenhuber, J. and
                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 544)
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BI455545 888 bp mRNA linear EST 21-AUG-2001 603173974F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5253090 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 3' sequence of the clone insert Clone from S. Wlemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wlemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., sequenced by GBF (National Research Centre for Biotechnology Ltd.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone (DKFZp434D2317) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                German Genome Project
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/lab_host="DH10B"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: Not1; Site_2: SalI"
/note="Vector: pSport1; 316_1: Not1; Site_2: SalI"
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/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
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                  CTCCGGAGGGTGCTGGTCGGACACCGAGCTGCTGTCAATGTTGTAGACTTTGATGACAAG 1272
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  CTCAGGAGGGTGCTGGGGACACCGAGCTGCGGTCAATGTTGTAGACTTTGATGACAAG
                                                                          ACCTGTTCCAAAGACCGTTCCATCGCTGTGTGGGATATGGCTTCCCCAACTGACATCACC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BI455545
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High quality sequence stop: 684
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Clone distribution: MGC clone distribution information can
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5253090"
/clone_lib="NCI_CGAP_Mam5"
/tion:
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/dev_stage="7 months"
/lab_host="DH10B"
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Search completed: February 22, 2003, 00:36:50 Job time: 2816 secs



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1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.8	1.8	1.8	1.8	1.8
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Sequence 473, App	Sequence 473, App	Sequence 473, App	~	•	Sequence 476, App	Sequence 476, App	•	Sequence 476, App	Sequence 476, App	Sequence 14, Appl	Sequence 1, Appli	Sequence 5, Appli	Sequence 266, App	Sequence 119, App		Sequence 348, App		Sequence 242, App	Sequence 67, Appl	Sequence 218, App	Sequence 1690, Ap	Sequence 317, App	Sequence 101, App	Sequence 1196, Ap	Sequence 97, Appl

ALIGNMENTS

RESULT 1 US-10-042-417-1 US-10-042-417-1 GENERAL INFORMATION: APPLICANT: Pagano, METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS FILE REFERENCE: 5914-090-999 Sequence 1, Application US/10042417 Patent No. US20020123082A1 Matches 2151; Query Match Best Local : SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1 CURRENT APPLICATION NUMBER: US/10/042,417 CURRENT FILING DATE: 2002-01-07 PRIOR APPLICATION NUMBER: 60/260,179 PRIOR FILING DATE: 2001-01-5 NUMBER OF SEQ ID NOS: 89 LENGTH: 2151 TYPE: DNA ORGANISM: Homo sapiens Local Similarity Conservative 100.0%; Score 2151; 100.0%; Pred No. 0; 0 Mismatches 0 DB 12; Length 2151; 0, Indels 0; Gaps 0; S S

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TTTGATGACAAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTATGGAACACA
                                                                                                                ACTGACATTACCCTCCGGAGGGTGCTGGTCGGACACCGAGCTGCTGTCAATGTTGTAGAC
                                                                                                                                                                                GGCATGATGGTGACCTGCTCCAAAGATCGTTCCATTGCTGTATGGGATATGGCCTCCCCA
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US-10-023-530-1
US-10-023-530-1
Sequence 1, Application US/10023530
Publication No. US20030007956A1
GEMERAL INFORMATION:
APPLICANT: LEGRAIN, Pierre
APPLICANT: BENAROUS, Richard
APPLICANT: BLOT, Guillaume
APPLICANT: HASSOT, Irina
TITLE OF INVENTION: PROTEINS THAT INTERACT WITH
FILE REFERENCE: B4717A
CURRENT APPLICATION NUMBER: US/10/023,530
CURRENT FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/256,276
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 30
SOSTWARE: Patentin version 3.1
SEQ ID NO 1
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; LOCATION: (1)..(657)
; OTHER INFORMATION: Beta TrCP
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Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
                                                                                  GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ08
                                                                                                                                        Sequence 15, Application US/09764848 Patent No. US20020077270A1
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                                                        CURRENT APPLICATION NUMBER: US/09/764,848
CURRENT FILING DATE: 2001-01-17
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NAME/KEY: SITE
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1018 GAGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGATGTAAATACA 107
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nes 597; Conserv
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                                              TTGGAATGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCCTCTGTCTCTCCAGTATGAT
                                                                                                            TTACAGAGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGTTTACAGTATGAT
                                                                                                                                                                                                                  CCAAAGATTATCCAGGATATAGAGACTATAGAATCTAACTGGCGGTGTGGACGACACAC
                                                                                                                                                                                                                                     CCTAAAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGTGGAAGACATAGT
                                                                                                                                                                                                                                                                                                                                           GTCAGGACAGATTCTCTGTGGAGAGGGCCTGGCAGAACGAAGGATGGGGACAGTATTTA
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                              CTGGAATGTTTGAAAGTGTTWACAGGACACACACGCTCTGK-CTCTGTCTGCAGTATGAT
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Pred. No. 3.4e-123;
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                                                                                                                                                                                                                                     SEQ ID NO 2778
LENGTH: 479
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PRIOR EILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION OF 1000-05-26
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                                                                                                                                                                                                                                                                          SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 49117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                       ORGANISM: Homo sapiens FEATURE:
                                                               OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                             OTHER INFORMATION: OTHER INFORMATION:
                                                OTHER
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    R INFORMATION: R INFORMATION: R INFORMATION:
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00666
FILIM DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
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                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 09/774,203
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APPLICATION NUMBER: US 09/608,408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00670
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APPLICATION NUMBER: PCT/US01/00661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00663
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N: MAP TO APO00252.1

N: EXPRESSED IN HBLLO, SIGNAL = 3.4

N: EXPRESSED IN LUNG, SIGNAL = 3.1

N: EXPRESSED IN HELA, SIGNAL = 3.1

N: EXPRESSED IN BP474, SIGNAL = 2.8

N: EXPRESSED IN BONE MARROW, SIGNAL = 0.6

N: EXPRESSED IN PLACENTA, SIGNAL = 1.6

N: EXPRESSED IN HEART, SIGNAL = 1.6
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US-09-864-761-19492/c

: Sequence 19492, Application US/09864761

: Patent No. US20020048763A1
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Best Local Similarity
Matches 359; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                        PRIOR PRIOR
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PRIOR APPLICATION NUMBER: US
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CURRENT FILING DATE: 2001-05-23
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                   APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
                                                                     APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
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EXPRESSED IN FETAL LIVER, SIGNAL
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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                                   TGTGAATTTGTAAGGACCTTAAATGGACACAAACGAGGCATTGCCTGTTTGCAGTACAGG 1386
                                                                               GAGAAATACATCGTGTCTGCCTCTGGTGACAGGACCATCAAAGTCTGGAGCATGAGCACC 70
                                                                                                    GACAAGTACATTGTTTCTGGATCTGGGGATAGAACTATAAAGGTATGGAACACAAGTACT 1326
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TGTGAATTTGCTCGTACTCTCAATGGGCACAAGCGAG----
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EXPRESSED IN BRAIN, SIGNAL = 4.3
EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
NT HIT: ABO14596.1, EVALUE 0.00e+00
EST_HUMAN HIT: ALO40743.1, EVALUE 1.00e-102
SMISSPROT HIT: Q91854, EVALUE 3.00e-46
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74.3%;
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D IN LUNG, SIGNAL = 2.6

D IN HELA, SIGNAL = 3.1

D IN BT474, SIGNAL = 2.8

D IN BONE MARROW, SIGNAL = 0.6

D IN PLACENTA, SIGNAL = 1.6
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Pred. No. 9.4e-54;
0; Mismatches 91; 1
--TCTTGTCTCCAGTACAGG
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; LOCATION: (261)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 13-LIB3058-049-Q1-K1-D1
US-09-960-352-2934
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                     SEQ ID NO 20
LENGTH: 1881
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APPLICANT: Tao, Nengbing
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
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                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application US/09213888A Patent No. US20020164683A1
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                                                                                                                                                                            APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Set-10 Polypeptides and Polynucleotides
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
                                                                                                            CURRENT APPLICATION NUMBER: US/09/213,8888 CURRENT FILING DATE: 1998-12-17 NUMBER OF SEQ ID NOS: 27
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                                                                                       SOFTWARE: PatentIn Ver. 2.0
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ORGANISM: Artificial Sequence
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Similarity 93.1%;
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US-09-328-877A-20
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; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: homo sapiens
US-09-213-888-20
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                                                                                     GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: L1, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides
TITLE OF INVENTION: Encode Them
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Best Local
                    FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877A
CURRENT FILING DATE: 1999-06-09
NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1033
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SEQ ID NOS: 27
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Sequence 26, Application US/09213888A
Patent No. US20020164633A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
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OTHER INFORMATION: Description of OTHER INFORMATION: homo sapiens
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; OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: homo sapiens US-09-213-888-26
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Pred. No. 2.1e-27;
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RESULT 10
US-09-328-877A-26
; Sequence 26, Application US/09328877A
; Patent No. US20020177187A1
; GENERAL INFORMATION:

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; OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: homo sapiens US-09-328-877A-26
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LENGTH: 2001
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APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polype
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
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CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
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Pred. No. 2.1e-27;
0; Mismatches 328;
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US-09-213-888-24
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CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
LENGTH: 2010
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APPLICANT: Li, Jinhe
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
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Local Similarity 50.2%;
es 340; Conservative
TTAACAAGTGGAATGGAACTCAAAGACAATATTCTTGTCTCTGGGAATGCAGATTCTACA 1566
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Pred. No. 2.1e-27;
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US-09-328-877A-24
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CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
LENCTH: 2010
TYPE: DNA
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APPLICANT: Gurney, mark E.
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Best Local Similarity
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APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
1447 ATCCGTGTTTGGGATGTGGAGACAGGGAATTGCATTCACACGTTAACAGGGCACCAGTCG 1506
                                                    1423 ATCAGATTATGGGACATAGAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAA 1482
                                                                                                     1387 AGAGTCTATTCATTACAGTTTGATGGTATCCATGTGGTGAGTGGATCTCTTGATACATCA 1446
                                                                                                                                                                                                          1327 GTAAAGGTGTGGGATCCAGAGACTGAAACCTGTCTACACACGTTGCAGGGGCATACTAAT 1386
                                                                                                                                                                                                                                                            1303 ATAAAGGTATGGAACACAAGTACTTGTGAATTTGTAAGGACCTTAAATGGACACAAACGA 1362
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; LOCATION: (3372)
US-09-213-888-1
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APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
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Best Local Similarity
Matches 340; Conserv
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APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
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ORGANISM: Homo sapiens
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GTAAAGGTGTGGGATCCAGAGACTGAAACCTGTCTACACACGTTGCAGGGGCATACTAAT 1430
                                          ATAAAGGTATGGAACACAAGTACTTGTGAATTTGTAAAGGACCTTAAATGGACACAAACGA 1362
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Pred. No. 3.1e-27;
0; Mismatches 328;
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (2485)
; NAME/KEY: unsure
; LOCATION: (3372)
US-09-328-877A-1
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; LENGTH: 3550
; TYPE: DNA
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Best Local
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APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
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                                             TGGGATATGGCCTCCCCAACTGACATTACCCTCCGGAGGGTGCTGGTCGGACACCGAGCT 1242
                                                                                                                                                                                                                                            TGGGATGTAAATACAGGTGAAATGCTAAACACGTTGATTCACCATTGTGAAGCAGTTCTG 1122
                                                                                                                                                                                                                                                                                             TCATCACAAATGAGAGACAACATCATCATTAGTGGATCTACAGATCGGACACTCAAAGTG
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                                                                                              TGTATGCATCTTCATGAAAAAAGAGTTGTTAGCGGTTCTCGAGATGCCACTCTTAGGGTT
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US-09-213-888-2
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Best Local :
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LENGTH: 3571
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: unsure
LOCATION: (2506)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/213,888A CURRENT FILING DATE: 1998-12-17 NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
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1161 TGGAATGCAGAGACTGGAGAATGTATACACACCTTATATGGGCATACTTCCACTGTGCGT 1220
                                           1063 TGGGATGTAAATACAGGTGAAATGCTAAACACGTTGATTCACCATTGTGAAGCAGTTCTG 1122
                                                                                        1101 TCATCACAAATGAGAGACAACATCATTAGTGGATCTACAGATCGGACACTCAAAGTG
                                                                                                                   1003 TGTCTCCAGTATGATGAGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTG 1062
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                                                                                                                                                                                                                                                                                                                   883 TGTTTACAGTATGATGATCAGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATC 942
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                                                                                                                                                      TTGGTGCGTTGTATTCGATTTGATAACAAGAGGATAGTCAGTGGGGCCTATGATGGAAAA 1542
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Search completed: February 22, 2003, 02:00:32 Job time: 185 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /cgn2_6/ptodata/1,
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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US-08-190-802A-30
US-08-477-346-30
US-08-477-3089-30
US-08-487-072A-30
US-08-190-802A-32
US-08-190-802A-32
US-08-477-089-32
US-08-477-165A-29
US-08-190-802A-23
US-08-190-802A-23
US-08-190-802A-51
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Sequence 30, Appl
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Sequence 32, Appl
Sequence 32, Appl
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seducince to, ubbt	Secuence 18 April	Sequence 18, Appl	Sequence 16, Appl	Sequence 16, Appl	Sequence 2, Appli	Sequence 26, Appl	Sequence 2, Appli	Sequence 2, Appli		Sequence 62, Appl	Sequence 62, Appl	Sequence 3, Appli	Sequence 62, Appl	Sequence 5, Appli	Sequence 5, Appli	Sequence 6, Appli	•	Sequence 52, Appl

RESULT 1

ALIGNMENTS

US-08-190-802A-30 US-08-190-802A-30 Sequence 30, Application US/08190802A Patent No. 5519003 GENERAL INFORMATION: PILLING DATE: 01-FEB-1994 CLASSIFICATION: 530 ATTORNEY, AGENT INFORMATION: NAME: Fabian, Gary R. REGISTRATION NUMBER: 33,87! REFERENCE/DOCUMENT: 33,87! TELEFAX: (415) 324-096 INFORMATION FOR SEQ ID NO: TOPOLOGY: unknow... MOLECULE TYPE: peptide REFERENCE/DOCKET NUMBER: 861 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 324-0880 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: ZIP: 94306-0850 COMPUTER READABLE FORM: APPLICANT: Mochly-Rosen, Daria APPLICANT: Ron, Dorit TITLE OF INVENTION: WD-40 - De TITLE OF INVENTION: Thereof HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: SEQUENCE CHARACTERISTICS: \ LENGTH: 517 amino acids STATE: C COMPUTER: IBM PC OPERATING SYSTEM: STREET: P.U. LU. CITY: Palo Alto MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS APPLICATION NUMBER: US/08/190,802A FILING DATE: 01-FEB-1994 INDIVIDUAL ISOLATE: TYPE: amino acid ADDRESSEE: CA P.O. Box 60850 (415) 324-0960 USA Dehlinger & WD-40 - Derived Peptides and BETA TRCP, Fig. 33,875 30: ON: Associates Score 2582.5; DB 1; Pred. No. 2.9e-266; Uses Length 517;

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18 SSEREDCHNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTKLAN 77

Query Match
Best Local Similarity
Matches 487; Conserv

Conservative

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85.1%; 91.4%;

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                           TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30
                                                                      APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: WD-40 - Derived Peptides and Uses TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mochly-Rosen, Daria APPLICANT: Ron, Dorit
                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Washington
STATE: DC
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COUNIN.
ZIP: 2006-181.
ZIP: 2006-181.
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             NUMBER OF SEQUENCES:
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STATE:

엉

CITY: Washington

STREET: ADDRESSEE:

2000 Pennsylvania Avenue, NW

Morrison & Foerster

Thereof

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US-08-473-089-30
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                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                     APPLICANT: Mochly-Rosen, Daria APPLICANT: Ron, Dorit
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HYPOTHETICAL: N
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LENGTH: 517 amino acid
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91.4%;
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Pred. No. 2.9e-266;
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to be property
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                                                                Sequence 30, Application US/08487072A Patent No. 6423684
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE JOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
             APPLICANT: Mochly-Rosen, Daria APPLICANT: Ron, Dorit
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TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 07-JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 GTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLK 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                        TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ
                                                                                                                                                                                                                                                                                                                                                                                              QRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRVLMGHTGSVLCLQYDE
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                                                                                                                                                                             VAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDP 514
                                                                                                                                                                                                                                                  YRDRLYVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL
                                                                                                                                                                                                                                                                                                                                                          TDITLRRYLYGHRAAVNYVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ 437
                                                                                                                                                                                                                                                                                                                                                                                                                                   RVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTDSLWRGLAERRGWGQYLFKNKPPDGKTPPNSFYRALYPKIIQDIETIESNWRCGRHSL
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91.4%;
WID-40 - Derived Peptides and Uses
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Pred. No. 2.9e
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Best Local S
Matches 487
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SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acid
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MOLECULE TYPE:
HYPOTHETICAL: N
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPHOX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                402 YRDRLYVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL 461
                                                  438 YRDRLYVSGSSDNTIRLWDIECGACLRYLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL 497
                                                                                        342 TDITLRRYLYGHRAAVNYVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ
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TORNEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 SSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTKLAN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
                                                                                                             TDITLRRVLYGHRAAVNVVDEDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ 437
                                                                                                                                                                                                                                                      QRIHCRSETSKGYYCLQYDDQKIYSGLRDNTIKIWDKNTLECKRILTGHTGSYLCLQYDE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLK 137
                                                                                                                                                                                                                                   QRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRVLMGHTGSVLCLQYDE
                                                                                                                                                                                                                                                                                                         RTDSLWRGLAERRGWGQYLFKNKPPDGKTPPNSFYRALYPKIIQDIETIESNWRCGRHSL
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                                                                                                                                                                                                                                                                                                                                                                                                                  PMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTSSMIVPKQRKLSANYEKEKELCVKYFEQWSECDQVEFVEHLISRMCHYQHGHINTYLK 102
                                                                                                                                                                RVIITG-SDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASA 341
                                                                                                                                                                                                RVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASP 377
                                                                                                                                                                                                                                                                                                                                           RIDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSL 257
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al Similarity 91.48;
487; Conservation-
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Pred. No. 2.9e-266;
7; Mismatches 8;
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; ORGANISM: Saccharomyces cerevisiae
US-09-177-165A-30
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US-09-177-165A-30
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Best Local Similarity
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PRIOR FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/177,165A
CURRENT FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/092,443
PRIOR FILING DATE: 1998-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Willems, Andrew
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
TITLE OF INVENTION: DEPENDENT PROTEOLYSIS
FILE REFERENCE: 11757.1005U1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tyers, Mike APPLICANT: Willems, A
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                                                                                                                                                                                                                                                                                                                                                                                                                       350
             583 -----KCMHTF---NGR--RLQRETQHTQTQSLGDKV 609
                                                            504 RAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTI 541
                                                                                                              526 LSCGLDNTIKLWDVKTGKCIRTQFGHVEGVWDIAADNFRIISGSHDGSIKVWDLQSG---
                                                                                                                                                                                                               466 VQKIIPLTIKDVENLATDNTSDGSSPQDDPTMTDGADESDTPSNEQETVLDENIPYPTHL
                                                                                                                                                                                                                                                                 430 KRGIACLQYRD--RLVVSGSS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292 --HCRIQEFKGHMDGVLTLQFNYRLLFTGSYDSTIGIWDLFTGKLIRRLSGHSDGVKTLY 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 RIHCRSETSK----GVYCLQYDDQKTVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQ 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 ---GWGQYLFKNK------PPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQ 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 --QELSLKILSYLDCQSLCNATRVCRKWQKLADDDRVWYHMCEQHI-----DRKC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 GLDHIAENILSYLDAKSLCAAELYCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERR- 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 PNCGWGLPLLHMKRARIQQNSTGSSSNADIQTQTTRPWKVIYRERFKVESNWRKG----- 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 NSNDKIRKL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 IPEKNSLRQTYNSCARLCLN-QETVCLASTAMKTENCVAK-TKLANGTSSMIVPKQRKLS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 LPEYNFTKFCYRHNPDIQFSPTHTACYKQDLKRTQEINANIAKLPLQEQSDIHHIISKYS 145
                                                                                                                                                                                                                                                                                                              ESRTCYTLR----GHTEWVNCVKLHPKSFSCFSCSDDTTIRMWDIRTNSCLKVFRGHVGQ 465
                                                                                                                                                                                                                                                                                                                                                             ASPTDITLRRVLVGHRAAVNVVDFDDKYI--VSASGDRTIKVWNTSTCEFVRTLNGH--- 429
                                                                                                                                                                                                                                                                                                                                                                                                            FDDRKLITGSLDKTIRVWNYITGECISTYRGHSDSVLSVDSYQKVIVSGSADKTVKVWHV 409
                                                                                                                                                           -----DNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDP 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-899-578-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 587 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 us-08-899-578-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 17.1%; Score 520; DB 3; Length 587; Best Local Similarity 28.8%; Pred. No. 2.4e-46; Matches 150; Conservative 78; Mismatches 222; Indels 70; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08899578 Patent No. 6087153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Greenwald, Iva
APPLICANT: Hubbard, E. Jane
TITLE OF INVENTION: SEL-10 AND USES THEREOF
                                          392 AVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDR--LVVSGSSD 449
                                                                                                                                                                                                                                                                                                                                                                                               151 SKNWKLISEIDKIWKSLGVEEFKHHPDPTDRVTGAWQGTAIAAG------VTIPDHIQP 203
380 AVRCVQFDGTTVVSGGYDFTVKIWNAHTGRCIRTLTGHNNRVYSLLFESERSIVCSGSLD 439
                                                                                                                                                                                             263 QIHDDVLVTGSDDNTLKVWCIDKGEVMYTLVGHTGGVWTSQISQCGRYIVSGSTDRTVKV 322
                                                                                                                                                                                                                                            274 QYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE--RVIITGSSDSTVRV 331
                                                                                                                                                                                                                                                                                                 204 CDLNVHRFLKLQKFGDIFERAADKSRYLRADKIEKNWNANPIMGSAV-LRGHEDHVITCM 262
                                                                                                                                                                                                                                                                                                                                                                                                                                              176 CKEWYRVTSDGMLWKKL-IERMV-----RTDSLWRGLAERRGWGQYLFKNKPPDGNAP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 FVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELV 175
                                                                                                                                                                                                                                                                                                                                                228 PN-SFYRALYPKIIQDI-------ETIESNWRCGRHSLQRIHCRSETSKGVYCL 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 ESSYSNGSSSSYNADKLSSSRPLQHKLDLSASPSRNNDLNPRVEHLIALFKDLSSAEQMD 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 KTKLANGTSSMI------VPKQRK--LSASYEKEKEL-----CVKYFEQWSESDQVE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/899,578
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1185 A CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
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                                                                                                 WSTVDGSLLHTLQGHTSTVRCMAMAGSILVTGSRDTTLRVWDVESGRHLA---TLHGHHA
                                                                                                                                           WDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFTRLLQESNMTNIRQLRAIIEPHFQRDFLSCLPV----ELGMKILHNLTGYDLLKVAQV 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
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278-0525
NO: 2:
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                                                                                                                                                                                                                                                                                                                      Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                          Query Match
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INFORMATION FOR SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               492 EGT-CVHMLSGHRSAITSLQWFGRNMVATSSDDGTVKLWD 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           440 TSIRVWDFTRPEGQECVALLQGHTSLTSGMQLRGNILVSCNADSHVRVWDI------H 491
332 NSLNLKLSQKYPKLSQQDRLRLSFLENIFILKNWYNPKFVPQRTTLRGHMTSVITCLQFE 391
                                   226 APPNSFYRALYPKIIQD-----IET--IESNWRCGRHSLQRIHCRSETSKGVYCLQYD 276
                                                                                                                                                                                                 109 SESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKS 168
                                                                                                                                                                                                                                        194 TTPLAKTTKTINN-----NNNIADLIESKDSIISPEYLSDEIFSAINNNLPHAYFK-- 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                               295 IINSLGVSQNWNKIIRKSTSLWKKLLISENFV-----
                                                                                                                   169 LCAAELVCKEWYR-VTSDGMLWKKLI--ERMVRTDSLWRGLAERRGWGQYLFKNKPPDGN 225
                                                                                                                                                           245 -----EISLKIFNYLQFED 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                              56 TYCLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEK-----ELCVKYFEQW 108
                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                         13.2%; Score 399;
24.3%; Pred. No. 3
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                                                                                                                                                                                                                                                                                                                      80; Mismatches 196; Indels 156; Gaps
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                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 779;
                                                                                   -----SPKGF 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Patent No.
        US-08-477-346-32
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                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                       TELEFAX: (202) 887-07 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20000 .... COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 -
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                ORIGINAL SOURCE:
                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 779 amino acids
                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     469 LDIVEYKNIKYIVTGSRDNTLHVWKLPKESSVPDHGEEHDYPLVFHTPEENPYFVGVLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           396 VDFDD----KYIVSASGDRTIKVWNT------STCE----FVRTLNG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 TGEMLNTLIHHCEAVLHLRENNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                392 DNYVITGADDKMIRVYDSINKKFLLQLSGHDGGVWALKYAHGGILVSGSTDRTVRVWDIK 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277 DQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE-RVIITGSSDSTVRVWDVN 335
                                                                 HYPOTHETICAL:
ANTI-SENSE: 1
                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              649 AADGSIRGWD-AND-----YSRKFSY 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  536 SHDDTILIWDFLNDPAAQAEPPRSPSRTYTY 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                487 AYDGKIKVWDL------VAALDPRAPAGTL--CLRTLVEHSGRVFRLQFDEFQIVSS 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             429 HKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN--KRIVSG 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                           TYPE: amino acid TOPOLOGY: unknow
                                                                                                                                                                                                                                                                                                         NAME: MURASHIGE, KATE H. REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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                         INDIVIDUAL ISOLATE: CDC4 / CDC20 protein, Fig.
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US-08-473-089-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
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APPLICANT: Ron, Dorit
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                                        APPLICATION NUMBER: FILING DATE: 07-JUI CLASSIFICATION: 43
                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Washington
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US-08-487-072A-32
                                                                                                                     Sequence 32, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                  APPLICANT: Mochly-Rosen, Daria APPLICANT: Ron, Dorit TITLE OF INVENTION: WD-40 - Dei TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                             589 SMDTTIRIWDLENIWNNGECSYATNSASPCAKILGAMYTLOGHTALVGLLRLSDKFLVSA 648
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INDIVIDUAL ISOLATE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 LCAAELVCKEWYR-VTSDGMLWKKLI--ERMVRTDSLWRGLAERRGWGQYLFKNKPPDGN 225
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                                     WD-40 - Derived Peptides and Uses
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LENGTH: 779 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
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MEDIUM TYPE: Floppy disk
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NAME: MURASHIGE, KATE H.
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 TVCLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEK-----ELCVKYFEQW 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                          LDIVEYKNIKYIVTGSRDNTLHVWKLPKESSVPDHGEEHDYPLVFHTPEENPYFVGVLRG
                                                                                                                                                                                              KG------HVFEGHNSTVRC
                                                                                                                                                                                                                                   TGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV
                                                                                                                                                                                                                                                                                                                                           NSLNLKLSQKYPKLSQQDRLRLSFLENIFILKNWYNPKFVPQRTTLRGHMTSVITCLQFE
                                                                                                                                                                                                                                                                                                                                                                             APPNSFYRALYPKIIQD-----IET--IESNWRCGRHSLQRIHCRSETSKGVYCLQYD 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LCAAELVCKEWYR-VTSDGMLWKKLI--ERMVRTDSLWRGLAERRGWGQYLFKNKPPDGN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SESDOVEFVEHLISOMCHYOHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKS 168
                                                    HMASVRTVSGHGNIVVSGSYDNTLIVWDVAQMKCLYILSGHTDRIYSTIYDHERKRCISA 588
                                                                     HKRGIACLQYRDRLVVSGSSDNTIRLMDIECGACLRVLEGHEELVRCIRFDN--KRIVSG
                                                                                                                                                            VDFDD----KYIVSASGDRTIKVWNT-----
                                                                                                                                                                                                                                                                     DNYVITGADDKMIRVYDSINKKFLLQLSGHDGGVWALKYAHGGILVSGSTDRTVRVWDIK 451
                                                                                                                                                                                                                                                                                                       DQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE-RVIITGSSDSTVRVWDVN 335
                                                                                                                                                                                                                                                                                                                                                                                                               IINSLGVSQNWNKIIRKSTSLWKKLLISENFV----
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2000 Pennsylvania Avenue,
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24.3%; Pred. No. 3e-33;
---VAALDPRAPAGTL--CLRTLVEHSGRVFRLQFDEFQIVSS
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                                                                                                                                                              --STCE----FVRTLNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-177-165A-29
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SEQ ID NO 29
LENGTH: 779
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Patent No. 6426209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/177,165A CURRENT FILING DATE: 1998-10-22 PRIOR APPLICATION NUMBER: 60/092,443 PRIOR FILING DATE: 1998-07-10 PRIOR APPLICATION NUMBER: 60/063,254 PRIOR FILING DATE: 1997-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN TITLE OF INVENTION: DEPENDENT PROTECLYSIS FILE REFERENCE: 11757.10USU1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tyers, Mike APPLICANT: Willems, Andrew
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536 SHDDTILIWDFLNDPAAQAEPPRSPSRTYTY 566 : | : | | | | | | | | | | ::|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKS 168
                                                                                                                                                                            HKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIREDN--KRIVSG 486
                                                                                                                                                                                                                                          LDIVEYKNIKYIVTGSRDNTLHVWKLPKESSVPDHGEEHDYPLVFHTPEENPYFVGVLRG
                                                                                                                                                                                                                                                                                    VDFDD----KYIVSASGDRTIKVWNT-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSLNLKISQKYPKLSQQDRLRLSFLENIFILKNWYNPKFVPQRTTLRGHMTSVITCLQFE 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPNSFYRALYPKIIQD-----IET--IESNWRCGRHSLQRIHCRSETSKGVYCLQYD 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IINSLGVSQNWNKIIRKSTSLWKKLLISENFV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCAAELVCKEWYR-VTSDGMLWKKLI--ERMVRTDSLWRGLAERRGWGQYLFKNKPPDGN 225
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                                                                SMDTTIRIMDLENIWNNGECSYATNSASPCAKILGAMYTLQGHTALVGLLRLSDKFLVSA 648
                                                                                                            AYDGKIKVWDL------VAALDPRAPAGTL--CLRTLVEHSGRVFRLQFDEFQIVSS 535
                                                                                                                                                       HMASVRTVSGHGNIVVSGSYDNTLIVWDVAQMKCLYILSGHTDRIYSTIYDHERKRCISA
                                                                                                                                                                                                                                                                                                                                                                                                                       DNYVITGADDKMIRVYDSINKKFLLQLSGHDGGVWALKYAHGGILVSGSTDRTVRVWDIK 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE-RVIITGSSDSTVRVWDVN 335
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                                                                                                                                                                                                                                                                                                                                    ---CCT---
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                                                                                                                                                                                                                                                                                    ----STCE----FVRTLNG 428
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US-08-914-999-8
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ryazanov, Alexey G. APPLICANT: Hait, William N. APPLICANT: Pavur, Karen S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ELONGATION FACTOR-2 KINASE TITLE OF INVENTION: AND METHODS OF USE THEREFOR
        496
                                       249 NWRCGRHSLQRIHCRSETSKG----VYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILT 304
                                                                                                                                189
                                                                                                                                                                         453 ---
                                                                                                                                                                                                     129 HGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGML 188
                                                                                                                                                                                                                                                405 SRQLFVSNDGNTLNTNKERSKSKSIDLEKPEILIN--NKKKESINLETIK------ 452
                                                                                                                                                                                                                                                                                                                               345 LIFPDTSERDNUNUNUNUNUNUNUNUNUNUNUNUNUNUNUNUNUSSISKSLVEISSGSKERNDRDSP 404
                                                                                                                                                                                                                                                                                     73 TK---LANGTSSMIVPKORKLSASYEKEK-ELCVKYFEOWSESDQVEFVEHLISOMCHYO 128
                                                                                                                                                                                                                                                                                                                                                                        13 LKFMNSSEREDCNNGEPPRKTIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Dictyostelium discoideum
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Hackensack
STATE: New Jersey
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                                                                                                                     WKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIES 248
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201-343-1684
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24.1%; Pred. No. 1.5e-32;
ative 84; Mismatches 172; Indels 118; Gaps
-QTLKGHEGPVESICYNDQYLFSGSSDHSIKVWDLKKLRCIFTLE 539
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                                                                                                                                                                ----LIETIKGYHVTSHLC----IC-----DNLL 473
                                                                                    -YDYKS--
                                                                                ----QNMECV-- 495
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US-08-283-917-3
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Patent No. 584955
Query Match 11.7%; Score 354; DB 2; Length 409; Best Local Similarity 29.2%; Pred. No. 6.4e-29;
                                                                                                                                                                                                                            TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
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                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413 3000
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP 2: FILING DATE: 03-AUG-1993 ATTORNEY/AGENT INFORMATION: NAME: Oblon, No. 5849557
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MEDIUM TYPE: Floppy
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CURRENT APPLICATION DATA:
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                                                                                                                                              TOPOLOGY:
                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                       NAME: Oblon, No. 5849557man F. REGISTRATION NUMBER: 24,618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/283,917 FILING DATE: 03-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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                                                                                    ORGANISM:
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Indels

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; MOLECULE TYPE:
; ORIGINAL SOURCE:
; ORGANISM: BOS
US-08-961-716-3
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                                                                                                                                                              TELEFAX: (703) 413-222
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STREET: 1/2
CITY: Arlington
STATE: Virginia
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CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 03-AUG-1994
APPLICATION NUMBER: JF 2
FILING DATE: 03-AUG-1993
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                                                                                                                                                                                                                                                                                    NAME: Oblon, No. 5880272man F. REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2292-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/961,716 FILING DATE:
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                                                                                   TOPOLOGY:
                                                                                                    STRANDEDNESS:
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SYSTEM: PC-DOS/MS-DOS
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                     Bos taurus
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; MOLECULE TYPE: US-08-283-917-9
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GENERAL INFORMATION:
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Best Local (
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                                                                                                                       REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 209943/1993
FILING DATE: 03-AUG-1993
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 IVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE--RVIITGSSDSTVRVWDVNTG 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 VRPNQDGTLIASCSNDQTVRVWVVATKECKAELREHEHVVECISWAPESSYSSISEATGS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           396 V--DFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDR------- 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1755 S. CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity nes 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                              TOPOLOGY:
                                                                                                                                                                                                                                                   NAME: Oblon, No. 5849557man F. REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                    LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETKKSGKPGPFLLSGSRDKTIKMWDVSTGMCLMTLVGHDNWVRGVLFHSGGKFILSCADD 358
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                                          : 410 amino acids
amino acid
GY: linear
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INOUE, KEIZO
ARAI, HIROYUKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEUSTADT, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OBLON, SPIVAK, McCLELLAND, MAIER &
                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER: US/08/283,917
03-AUG-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -KNKRCMKTLNAHEHFVTSLDFHKTAPYVVTGSVDQTVKVWE 407
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Qy ₽ Qy Search completed: February 20, 2003, 09:56:08 Job time : 20 secs δÃ. 망 DЬ Qy В DЬ Query Match 11.7%; Score 354; DB 2; Length 410; Best Local Similarity 29.2%; Pred. No. 6.4e-29; Matches 87; Conservative 57; Mismatches 110; Indels 44; Gaps v 8; 338 EMINTLIHHCEAVLHLRF--NNGMMYTCSKDRSJAVWDMASPTDITLRRVLVGHRAAVNV 395

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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 SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria
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6: sp_mammal:*
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Gapop 10.0 , Gapext 0.5
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1 MDPAEAVLQEKALKFMNSSE......PAAQAEPPRSPSRTYTYISR 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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sp_fungi:*
               sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
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sp_mammal:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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16	16	13	12	11	10	9	8	7	6	5	4	ω	N	<u>, , , , , , , , , , , , , , , , , , , </u>	Result
639	640	640	640	640	640	661	1230	1498	2089.5	2089.5	2286	2978	2990	2997	Score
21.1	21.1	21.1	21.1	21.1	21.1	21.8	40.5	49.4	68.9	68.9	75.3	98.2	98.5	98.8	Query Match
629	707	627	589	561	553	1326	252	430	510	510	563	569	569	569	Length DB
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Q8vbv4 mus musculu	homo	Q96a16 homo sapien	homo	homo	Q9nux6 homo sapien	Q9vzf4 drosophila	Q922c7 mus musculu	Q9bj54 heterodera	Q9vde3 drosophila	O44382 drosophila	Q923h0 mus musculu	Q9r1g7 mus musculu	Q9z159 mus musculu	Q9qui5 mus musculu	Description

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587 1376 1356 1356 1356 1356 1227 1717 1718 1718 1718 1718 1718 1718	122
114415 114416 114416 1146 1146 1146 1146	113
044083 08X1P2 08X1P3 08X1P5 08X1P5 08X1P5 08X1P5 08X1P3 08X1P3 08X1P3 08Y1P3 09D4T2 08Y2D9 097D14 09PTR5 08W2D9 09CD15 08W2D9 09CD15 08W2D9 09CD15 08W2D9 09CD15 08W2D9 09CD15 08W2D9	QBUUN3
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ALIGNMENTS

R R R R	2 R R R	RN	2 Z	RT	R S	D RX	RP	R R	RT	RT.	RA	RA	0 7	RP	RN	0 X	ጸ	88	2 2	2 5	DE	DJ.	j [AC.	Ü	RESULT Q9QUI5
[4] SEQUENCE FROM N.A. STRAIN=129/SV; MEDLINE=21601157; PubMed=11735228;	SEQUENCE FROM N.A. Strausberg R.; Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.	[3]	nature 396:590-594(1998).	component of the	F. Ben-Neriah V.:	n	SEQUENCE FROM N.A.	Proc. Natl. Acad. Sci. U.S.A. 96:3859-3863(1999). [2]	Skp1/Cul 1/F-box protein FWD1.";	"Ubiquitin-dependent degradation of IkappaBalpha is mediated by a	a Ki.;	ashi H., Nakano H., Okumura K., Onoe K	Shirano M Matsumoto	SEQUENCE FROM N.A.	[1]		Rodentia; Sciurognathi; Muridae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	MIS TUSCULIUS (MOUSE)	(F-DOX-WD40 repeat protein i).	Ubiquitin ligase FWD1 (Beta-transducin repeat containing protein)	MBLrel. 20, Last annotation	Ol-MAY-2000 (IIEMBELTOI 13. Last socience indate)	American 13	Q9QUI5 PRELIMINARY; PRT; 569 AA.	1

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
PROSITE; PS50181; FBOX; 1.
PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_6.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50234; WD_REPEATS_REGION; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ligase; Repeat; WD repeat.
SEQUENCE 569 AA; 65105 MW;
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ProDom; PD000018; WD40; 4.
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Nakayama K.-
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                      EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN 480
                                                              VTCSKDRSIAVWDMASPIDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRIIKVWNTSTC 420
                                                                                                    RILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNAGEMLNTLIHHCEAVLHLRFNNGMM
                                                                                                                RILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMM 360
                                                                                                                                                                   QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK 300
EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN
                                                 VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC
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                                                                                                                                                                                                                     RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII 240
                                                                                                                                                                                                                                                                        ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180
                                                                                                                                                                                                                                                                                                        STAMKTENCVAKAKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
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AF391183;
AF391184;
AF391185;
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AF391178;
AF391179;
AF391180;
AF391181;
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AAL40929.1
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AAH03989.1; -.
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3; Mismatches
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Pred. No. 7
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Best Local
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PRODOM; PRO030018; WDA0; 4.
SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
PROSITE; PS50181; FBOX; 1.
PROSITE; PS50082; WD_REPEATS_1; UNKNOWN_6.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50084; WD_REPEATS_REGION; 1.
Repeat; WD repeat.
SEQUENCE 569 AA; 65047 MW; BC7C7A44815BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Signal-induced ubiquitination of IkappaBalpha Slimb/beta-TrCP,";
Genes Dev. 13:284-294(1999).
-!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP |
EMBL; AF112979; AAD04181.1; --
MGD; MGI:1338871; Btrc.
InterPro. Trees
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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01-MAY-1999 (TrEMBLICAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9Z159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001810; F-box. InterPro; IPR001680; WD40.
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       301
                               241
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                                                                                                                                                                                                                                                              1 MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60
                                                                                                                                                   ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180
RILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMM
                         QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKSTLECK
                                             QDIETIESNWRCGRHSLQRIHCRSETSKGYYCLQYDDQKIVSGLRDNTIKIWDKNTLECK 300
                                                                               RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII
                                                                                                                                    ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY
                                                                                                                                                                                          STAMKTENCVAKAKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL
                                                                                                                                                                                                         STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
                                                                                                                                                                                                                                              MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCINQETVCLT 60
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                                                                                                                                                                                                                                                                                                                                              repeat.
569 AA; 65047 MW; BC7C7A44815BED96 CRC64;
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.A.
                                                                                                                                                                                                                                                                                                                 98.5%; Score 2990; 98.4%; Pred. No. 2
                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                              .9e-252;
                                                                                                                                                                                                                                                                                                                              DB 11; Length
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SMART; SM00320; WD40; 7.

PROSITE; PS50181; FBOX; 1.

PROSITE; PS500878; WD_REPEATS_1; UNKNOWN_6.

PROSITE; PS50082; WD_REPEATS_2; 7.

PROSITE; PS50284; WD_REPEATS_REGION; 1.

Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Beta-transducin repeat-containing protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Winston J., Elledge S.J., Harper J.W.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9R1G7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00320; GPROTEINBRPT PRODOM; PD000018; WD40; 4.
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MGD; MGI:1338871; Btrc.
InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BTRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILIWDFLNDPAAHAEPPRSPSRTYTYISR 569
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                                                                                                                                                                                                                                                                                                                                  MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60
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                                                                                                                                                                                            STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL
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                                                                                                                                                                  STAMKTENCVAKAKLANGTSSMTVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL
RVTSDGMLWKKLIERMYRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII
                                                         ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHITENILSYLDAKSLCAAELVCKEWY
                                                                                  ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY
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                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65209 MW;
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                                                                                                                                                                                                                                                                                                                                                                                     Score 2978; DB 11;
Pred. No. 3.2e-251;
4; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 569;
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В
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                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                        Bhatia N., Herter J.R., Slaga T.J., Fuchs S.Y., Spiege
"Mouse homolog of HOS (mHOS) is overexpressed in skin
implicated in constitutive activation of NF kappaB.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ database
-! SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS
EMBL, AY038079; AAK72095.1; -.
EMBL, AY038079; AAK72095.1; -.
InterPro; IPR001810; F-box.
InterPro; IPR001810; F-box.
InterPro; IPR00180; WD40.
Pfam; PF00646; F-box; 1.
                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FBXWIB
                                                                                                                                                                                                                  Prodom; PD000018; WD40; 4.
PROSITE; PS500611; FBX; WD_REPEATS_1; UNKNOWN_5
PROSITE; PS50082; WD_REPEATS_2; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F-box/WD40 repeat-containing
                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                       Repeat; WD
                                                                                                                                                                                                    PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFVRTLNGHKRGIACLQYRDRLYVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK 300
 VRCLQNTSVMEDQNEDESPKKSALWQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYFDQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNAGEMLDTLTHHCEAVLHLRFNNGMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKSTLECK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDENAPPNSFYRALYPKII
                  TVCLASTA-MKTEN-----CVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQW 108
                                                         MEP-DSVIEDKTIELMCSVPRSLWLGCAN-----
                                                                                    MDPAEAVLQEKALKFMNSSERE----DCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQ--E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRIVSGRYDGKIKVWDLMAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT
                                                                                                                   440;
                                                                                                                               Similarity
                                                                                                                                                                           563
                                                                                                                                                                                       repeat
                                                                                                                75.3%; Score 2286; DB 11; ilarity 75.7%; Pred. No. 8e-191; Conservative 46; Mismatches 65;
                                                                                                                                                                           AA;
                                                                                                                                                                        64741 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein HOS.
                                                                                                                                                                           9AB562F3FF5E3496 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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                                                         -LVESMCALSCLQSMPS
                                                                                                                   Indels
                                                                                                                                            Length 563;
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   104
                                                                                                                   7;
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Best Local Similarity

78.38;

Pred.

No.

9.8e-174;

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ACCOMENS OF THE STATE OF THE ST
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     Query Match
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01-JUN-1998
01-JUN-1998
                                                                                                       PRINTS; PR00320; GPROTEINBRPT.
Probom; PD000018; WD40; 4.

SMART; SM00256; FBOX; 1.

SMART; SM00320; WD40; 7.

PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_5.

PROSITE; PS50082; WD_REPEATS_2; 7.

PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           Jiang J., Struhl G.;

Jiang J., Struhl G.;

Jiang J., Struhl G.;

Jiang J., Struhl G.;

Regulation of the Hedgehog and Wingless signalling pathways box/MDA0-repeat protein Slimb.";

Nature 391:493-496(1998).

In SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

EMBL; AF032878; AAC38852.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLIMB (
                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                        Pfam; PF00646; F-box;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98121115;    PubMed=9461217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFQIISSSHDDTILIWDFLNVPPSAQNETRSPFRTYTYISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLKTLVEHSGRVFRLOFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLVEHSGRVFRLQFD
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                                                                                                                                                                                                                                                                                                           PF00400; WD40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFQIVSSSHDDTILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPP
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                                                         58952 MW;
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20,
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Last annotation update)
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  Score 2089.5;
                                                      DBB0243D3730A5E8 CRC64;
DB 5;
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                                                                                                                                                                                                 Length 510
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                        Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottiter P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
                                                                                                                                                                                                                                                          MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
nallew B W Desn's A Baycasic T.
       Dodson K., Doup L.E., Downes M.,
Durbin K.J., Evangelista C.C., F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLMB protein (SLIMB).
SLMB OR CG3412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BERKELEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9VDE3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 HLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELYCKE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 MKTENCVAKTKLANG---TSSMIVPKQRKLSAS--YEKEKELCVKYFEQWSESDQVEFVE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 HLLSRMCHYQHGQINAYLKPMLQRDFITLLPIKGLDHIGENILSYLDAESLKSSELVCKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHD 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MMVTCSKDRSTAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTS 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CVKTLMGHTGSVLCLQYDDKVIISGSSDSTVRVWDVNTGEMVNTLIHHCEAVLHLRFNNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WLRVISEGMLWKKLIERKVRTDSLWRGLAERRNWMQYLFKPRPGQ-TQRPHSFHRELFPK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394;
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Last annotation updat
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   Ferraz C.,
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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassaman D.A., Weinstock G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhou X., Zhou X., Smith H.O.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhon, Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhon M., Zhang G., Zhou X., Smith H.O.,

RA Zheng X.H., Zhong F.N., Zhon G., Zhu X., Smith H.O.,

RA Zheng X.H., Zhong F.N., Zhon G., Zhu X., Smith H.O.,

RA Zheng X.H., Zhou S., Zhou X., Zhu X., Smith H.O.,

RA Zheng X.H., Zhong G., Zhong G., Zhong D.,

RA Zheng X.H., Zhong G., Zhong G., Zhong L.,

RA Zheng X.H., Wang S., Wang S., Zhou X., Smith H.O.,

RA Zheng X.H., Zhong G., Zhong G., Zhong L.,

RA Zheng X.H., Zhong G., Zhong G., Zhong L.,

RA Zheng X.H., Wang S., Zhou X., Zhu X., Smith H.O.,

RA Zheng X.H., Zhong G., Zhong G., Zhong L.,

RA Zheng X.H., Zhong G., Zhong H.,

RA Zheng X.H., Zhong G., Zhong G., Zhong L.,

RA Zheng X.H., Zhong G., Zhong M., Zhou X., Zhu X., Smith H.O.,

RA Zheng X.H., Zhong G., Zhong G
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Best Local (
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"Drosophila null slimb clones transiently deregulate Hedgehog-
independent transcription of wingless in all limb discs, and induce
decapentaplegic transcription linked to imaginal disc regeneration.";
Mech. Dev. 93:15;26(2000).

1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

EMBL; AE02073; AAF558531; -.

EMBL; AF222924; AAF63213.1; -.

EMBL; AF222923; AAF63213.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50181; FBOX; 1.

PROSITE; PS00678; WD_REPEATS_1; 5.

PROSITE; PS50082; WD_REPEATS_2; 7.

PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0023423; slmb.
InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00646; F-box; 1.
Pfam; PF00400; WD40; 7.
PRINTS; PR00320; GPROTEINBRPT.
PRODOm; PD000018; WD40; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=OVARY, AND IMAGINAL DISC; MEDLINE=20245299; PubMed=10781936;
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                                                          182
                                                                                                                                                                                                                                                                                                             119
                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                        64 MKTENCVAKTKLANG---TSSMIVPKQRKLSAS--YEKEKELCVKYFEQWSESDQVEFVE 118
                                                                                                                                                                                                                                                                                                                                                             4
     CKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNG
                                                                                                                                                         WLRVISEGMLWKKLIERKVRTDSLWRGLAERRNWMQYLFKPRPGQ-TQRPHSFHRELFPK 181
                                                                                                                                                                                 WYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPK 238
                                                                                                                                                                                                                                                                                                                                                             METDKIMDEIN-SNAQAFTTTMLYDPVRKKDSSPTYQTERELCFQYFTQWSESGQVDFVE
                                                       IMNDIDS I ENNWRTGRHMLRR I NCRSENSKGVYCLQYDDGK IVSGLRDNT I K IWDRTDLQ
                                                                                    IIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLE
                                                                                                                                                                                                                                                           HLLSRMCHYQHGQINAYLKPMLQRDFITLLPIKGLDHIAENILSYLDAESLKSSELVCKE
                                                                                                                                                                                                                                                                                                           HLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKE 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394;
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SM00320; WD40; 7.
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A., Gong F., Gorrell J.H., Gu Z., Guan P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WD repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.9%;
78.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2089.5;
Pred. No. 9.86
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kovaleva E.S., Yakovlev A.G., Masler E.P.;
"Plant parasitic nematode b-TRCP.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP
EMBL; AF339101; AAX26376.1; -.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heterodera glycines (Soybean cyst nematode)
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchoidea; Heteroderidae; Heteroderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9ВJ54
                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_6.
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00320; GPROTEINBRPT. ProDom; PD000018; WD40; 4. SMART; SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta-transducin repeat-containing protein (Fragment).
                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=51029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242
 417
                               181
                                                           357
                                                                                         121
                                                                                                                                                                                 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302
                                                                                                                                                                                                                                           193 IERMVRTDSLWRGLAERRGWGQYLFKNK-------PPDGNAP---PNSFYRALY 236
                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTILIWDFLNFTPNENKTGRTPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWN
                                                                                                                                                                     PKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DTKRIVSGAYDGKIKVWDLVAALDPRAASNTLCLNTLVEHTGRVFRLQFDEFQIVSSSHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MMVTCSKDRSIAVWDMTSPSEITLRRVLVGHRAAVNVVDFDEKYIVSASGDRTIKVWSTS
 TSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCI
                               DGMLVTCSKDRSIAVWDMASPRDIEVRRVLVGHRAAVNVVDFDHKYIVSASGDRTIKVWN
                                                                                         LGCVQTLSGHTGSVLCLQYDNQMIASGSSDATVRIWDVNTGEQLKTLVHHCEAVLHLRFQ 180
                                                                                                                     LECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFN 356
                                                                                                                                                   PKITADIRQIEQNWREGRHRLERINCQSENSKGVYCLQYDDEKIISGLRDNTIKIWSRPS 120
                                                                                                                                                                                                              IERQVRNDALWAGLAIRRGWKKYFFCSKDQATRAISQSWRQPKNGEDALEFQHKFYRELY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DTILIWDFLNDPAAQAEPPRSPS
                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                     430 AA;
                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                     47916 MW;
                                                                                                                                                                                                                                                                                         49.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17, Created)17, Last sequence update)20, Last annotation update)
                                                                                                                                                                                                                                                                         36;
                                                                                                                                                                                                                                                                                         Score 1498; DB 5;
Pred. No. 3.2e-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chromadorea; Tylenchida; Tylenchina;
                                                                                                                                                                                                                                                                                                                                     4ABC3FF2DFE3A50B CRC64;
                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                      .2e-122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heterodera
                                                                                                                                                                                                                                                                         50;
                                                                                                                                                                                                                                                                                                      Length 430;
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Q9VZF4
ID Q9
AC Q9
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                                                                       RESULT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              Matches
  Q9VZF4;
01-MAY-2000
01-MAY-2000
                                           Q9VZF4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00320; GPROTEINERPT.
PRODOM; PD000018; WD40; 3.
PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_5.
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to f-box and WD-40 domain protein 1B (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; BC008552; AAH08552. MGD; MGI:2144023; Fbxw1b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001680; WD40. Pfam; PF00400; WD40; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FBXW1B
                                                                                                                                                                                                                                                                                                                   318 RVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMAVTCSKDRSIAVWDMASP 377
                                                                                                                                                                181
                                                                                                            241 RSPSRTYTYISR 252
                                                                       و
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                                                                                                                                                                                                                                                                       61
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L; BC008552; AAH08552.1; -.
                                                                                                                                                           QAALDPRAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILLIMDFLNVPPSAQNET
                                                                                                                           RSPSRTYTYISR 569
                                                                                                                                                                                   VAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDPAAQAEPP 557
                                                                                                                                                                                                                            YRDRLYVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL 497
                                                                                                                                                                                                                                                                                TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ 437
                                                                                                                                                                                                                                                                TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWSTSTCEFVRTLNGHKRGIACLQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFDSKRIVSGAYDGKIMIMDLAAALDPMTPPNSICIKTLSQHTGRVFRLQFDEFQIISSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASTCEFVRTLNGHKRGIACLQYRDRLIVSGSSDYSIRLWDIECGNCLRVLEGHEELVRCI 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSS 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HDDTILIWDFLN-DPAA-------QAEPPRSPS 561
                                                                                                                                                                                                                                                                                                                                                                              234;
                                                                                                                                                                                                                                                                                                                                                                                                                                252 AA;
  (TrEMBLrel. 13, (TrEMBLrel. 13,
                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                28424 MW;
                                                                                                                                                                                                                                                                                                                                                                                      40.5%; Score 1230; 92.9%; Pred. No. 3
  Last sequence update)
                Created)
                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                           1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                       3.6e-99;
                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 252;
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                                                                                                                                                                                                                                                                                                                                                                           Indels
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 Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                               Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George Gonzalez M., Guarin H., Li P., Liao G., Minada A., Mungall C. Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wa Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                       Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.-!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS). EMBL; AE003480; AAG22246.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.
                                                              Celniker S.;
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tarcheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                           STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, Last annotation update) CG15010 protein (LD21322p) (LD30271p). AGO OR CG15010.
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BERKELEY;
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AAL28848.1;
AAL68231.1;
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Q9NUX6
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Best Local
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Pfam; PF00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00678; WD_REPEATS_1; 5.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
REPEAT; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
PROSITE; PS50181; FBOX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00646; F-box; 1 Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0041171; ago. InterPro; IPR001810; F-box
                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ11071 fis, clone PLACE1004937, moderately s:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1004
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Su
Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa
Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J.,
Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                       Q9NUX6;
                                                                                                                                                                                                                                                                                                            Q9NUX6
                                                                                                                                                                                                                                                                                                                                                                                                    1232 SGPNKHHSAVTCLQFNSRFVVTSSDDGTVKLWD 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 DAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPP-- 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        852 FQRWSHVERLLALDRLIDHCDPSQVRHMMKVIEPQFQRDFISLLPR----ELALFVLSYL 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 FEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYL 164
                                                                       FISSUE-PLACENTA;
                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVN 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPKDLLRAAQTCRSWRFLCDDNLLWKEKCRKA-----QILAEPR-----SDRPKRG 953
                                                                                                                                                                                                                                                                                                                                                                                                                                   V---EHSGRVFRLQFDEFQIVSSSHDDTILIWD 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLW 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGNRIVSGSDDNTLKVWSAVNGKCLRTLVGHTGGVWSSQMSGNIIISGSTDRTLKVWDMD 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RDGNMPPIASPWKAAYMR--QHI--IEMNWR-----SRPVRKPKVLKGHDDHVITCLQF 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -DGNAPP-NSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKG-----YYCLQY 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVETGNCKHTLMGHQSLTSGMELRQNILVSGNADSTVKVWDITTG-----QCLQTL 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIECGACLRVLEGHEELVRCIREDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTL 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQYDGKLIVSGAYDYMVKIWHPERQECLHTLQGHTNRVYSLQFDGLHVVSGSLDTSIRVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGACVHTLQGHTSTVRCMHLHGSKVVSGSRDATLRVWDIEQGSCL---HVLVGHLAAVRC 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1326 AA; 141360 MW; 3F42C873CFA3027F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.8%; Score 661; 34.9%; Pred. No. :
                                                                                                                                                                                                                     PLACE1004937, moderately similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76;
                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 167;
                                                                                                                                                                                                                                                                                                               553
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                      J., Wakamatsu
                                                          Suzuki Y.,
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                                                                                                                                                                                                                                                                                   Вb
   SS DT DT AC
                                                                                                                                   Q96RI2
                                                                                                                                                  RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
EMBL; AK001933; BAA91986.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50181; FBOX; 1.

PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_5.

PROSITE; PS50082; WD_REPEATS_2; 7.

PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pfam; PF00646; F-box; 1.
Pfam; PF00400; WD40; 7.
PRINTS; PR00320; GPROTEINBRPT
PRODOm; PD000018; WD40; 2.
 Q96RI2;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
F-box protein FBX30 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat; WD repeat.
Homo sapiens (Human).
                                                                                                                 Q96RI2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 MMQVIEPQFQRDFISLLP----KELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWRE
                                                                                                                                                                                                                                                                                                                                                               384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 LIERMVRTDSLWRGLAE-----RRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 INSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKK 191
                                                                                                                                                                                                              495
                                                                                                                                                                                                                                                                                   444 NADSTVKIWDIKTG------QCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 KFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLDHGSEVRSFSLGKKPCKV-----SEYTSTTGL-----VPCSA-----TPTTFGDL
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                                                                                                                                                                                                                                                                                                                       AYDGKIKVWDLVAALDPRAPAGTLCLRTLV----EHSGRVFRLQFDEFQIVSSSHDDTILI 543
                                                                                                                                                                                                                                                                                                                                                               QGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSG
                                                                                                                                                                                                                                                                                                                                                                                                 NGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKD 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTNWRRGELKSPKV-LKGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KCKE-----EGIDEPLHIKRRK-----VIKPGFIHSPWKSAY-----IRQ--HRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAANGQG-----QQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167;
                                                                                                                                                                                                                                                                                                                                                                                                                                        ATLRVWDIETGQCL---HVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWDPETETCLHTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                              496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                553 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62280 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 640; DB 4;
Pred. No. 3.6e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA829C221986A3F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 211;
                                         update)
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Matches
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Pfam; PF00400; WD40; 7.

ProDom; PD0000018; WD40; 2.

PROSITE; PS50181; FB0X; 1.

PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_5.

PROSITE; PS50082; WD_REPEATS_2; 7.

PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                             503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koepp D.M., Winston J.T., Harper J.W., Elledge S.J.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
'- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
EMBL, AF383178; AAK60269.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20003061; PubMed=10531037; Winston J.T., Koepp D.M., Zhu C., Elledge S.J., Harper J.W.; "A family of mammalian F-box proteins."; Curr. Biol. 9:1180-1182(1999).
                                                                                                                       544 WD 545
                                                                                                                                                                                             487 AYDGKIKVWDLVAALDPRAPAGTLCLRTLV---EHSGRVFRLQFDEFQIVSSSHDDTILI 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 ESNWRCGRHSLQRIHCRSETSKGYYCLQYDDQKIYSGLRDNTIKIWDKNTLECKRILTGH 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 KCKE-----EGIDEPLHIKRRK-----VIKPGFIHSPWKSAY-----IRQ--HRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001810; F-box. InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 LIERMVRTDSLWRGLAE-----RRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 MMQVIEPQFQRDFISLLP----KELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWRE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 INSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKK 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 RAANGQG-----QQRRKITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 KLANGTSSMIVPKORKLSASYEKEKEL -- CVKYFEQWSESDQVEFVEHLISOMCHYOHGH 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 KLDHGSEVRSFSLGKKPCKV-----SEYTSTTGL-----VPCSA-----TPTTFGDL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 KFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                   NADSTYKIWDIKTG------QCLQTLQGPNKHQSAYTCLQFNKNFYITSSDDGTYKL
                                                                                                                                                                                                                                          QGHTNRVYSLQFDGTHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSG
                                                                                                                                                                                                                                                                                                                                ATLRVWDIETGQCL---HVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWDPETETCLHTL
                                                                                                                                                                                                                                                                                                                                                                          RSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGSVLCLQYDERVIITGSSDSTYRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DTNWRRGELKSPKV-LKGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGH
                                                                                                                                                                                                                                                                                    NGHKRGIACLQYRDRLVYSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSG 486
                                                                                                                                                                                                                                                                                                                                                                                                                       TGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63165 MW; B81CC1E2206B0D88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.1%; Score 640; DB 4; 30.8%; Pred. No. 3.7e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001810; F-box.
InterPro; IPR001810; WD40.
Pfam; PP00646; F-box: 1.
Pfam; PP00646; WD40; 7.
Pfam; PP00400; WD40; 7.
ProDom; PD000018; WD40; 2.
PROSITE; PS50181; FB0X; 1.
PROSITE; PS0078; WD_REPEATS_1; UNKNOWN_5.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
480 NADSTVKIWDIKTG------QCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKL
                                          487 AYDGKIKVWDLVAALDPRAPAGTLCLRTLV---EHSGRVFRLQFDEFQIVSSSHDDTILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat; WD repeat.
SEQUENCE 589 AA; 66120 MW; 2AFB6E8A36E6E8DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li J., Pauley A.M., Myers R.L., Snuang K., Blashlet U.N., Lim N., Buhl A.E., Gurney M.E.; Buhl A.E., Gurney M.E.; "SEL-10 Interacts with Presentlin 1, Facilitates Its Ubiquitination, and Alters A-beta Production.";
                                                                                                                                                                                             363
                                                                                                                                                                                                                       367 RSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS) EMBL; AY008274; AAG16640.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TremBLrel 19, 01-DEC-2001 (TremBLrel 19, 01-JUN-2002 (TremBLrel 21,
                                                                                                                                                                                                                                                                      303 TGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRD
                                                                                                                                                                                                                                                                                                              307 TGSVLCLOYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKD
                                                                                                                                                                                                                                                                                                                                                          244 DTNWRRGELKSPKV-LKGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGH
                                                                                                                                                                                                                                                                                                                                                                                      247 ESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 KCKE-----EGIDEPLHIKRRK-----VIKPGFIHSPWKSAY-----IRQ--HRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 INSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 LIERMVRTDSLWRGLAE-----RRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F-box protein SEL10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q96LE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q96LE0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 KLANGTSSMIVPKORKLSASYEKEKEL--CVKYFEOWSESDOVEFVEHLISOMCHYOHGH 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 KLDHGSEVRSFSLGKKPCKV-----SEYTSTTGL-----VPCSA-----TPTTFGDL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 KFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                      QGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSG
                                                                                                                                NGHKRGIACLOYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSG
                                                                                                                                                                               ATLRYWDIETGQCL---HVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWDPETETCLHTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MMQVIEPQFQRDFISLLP----KELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAANGQG-----QQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity
167; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.1%; Score 640; DB 4
30.8%; Pred. No. 4e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92; Mismatches 211; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB_4; Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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Gaps

15;

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479

302 306 243

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RESULT
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EMBL; AF411972; AAL06291.1; -.

REMBL; AY03353; AAK57547.1; -.

RINTERPO; IPR001810; F-box.

InterPro; IPR001810; F-box.

RINTERPO; IPR001680; WD40.

REPORT : PR00400; WD40; 7.

REPORT : PR00400; WD40; 7.

REPORT : PR004018; WD40; 2.

REPORT : PS0078; WD_REPEATS_1; UNKNOWN_5.

REPORT : PS00794; WD_REPEATS_2; 7.

REPORT : PS00794; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                              Matches
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MEDLINE-21449047; PubMed-11565033;

MEDLINE-2149047; PubMed-11565033;

Moberg K.H., Bell D.W., Wahrer D.C., Haber D.A., Hariharan I.K.;

"Archipelago regulates Cyclin E levels in Drosophila and is mutated human cancer cell lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Archipelago beta form (F-box protein FBW7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Winston J.T., Koepp D.M., Zhu C., Elledge S.J., "A family of mammalian F-box proteins."; Curr. Biol. 9:1180-1182(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Koepp D.M., Winston J.T. submitted (APR-2001) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=20003061; PubMed=10531037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Local Similarity
                                                                                                                                                                                                                                                   KFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKT
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                                                                                                                                                                                                     KLANGTSSMIVPKQRKLSASYEKEKEL - - CVKYFEQWSESDQVEFVEHLISQMCHYQHGH
DTNWRRGELKSPKV-LKGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGH
                            ESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGH
                                                           KCKE-----
                                                                                     LIERMVRTDSLWRGLAE-----RRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETI
                                                                                                                  MMQVIEPQFQRDFISLLP----KELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWRE
                                                                                                                                  INSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKK
                                                                                                                                                                          RAANGQG-----QQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKH
                                                                                                                                                                                                                                  KLDHGSEVRSFSLGKKPCKV-----SEYTSTTGL-----VPCSA-----TPTTFGDL
                                                                                                                                                                                                                                                                                              167;
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E 627 AA; 70324 MW;
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                                                                                                                                                                                                                                                                                            Conservative
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                                                         -EGIDEPLHIKRRK-----VIKPGFIHSPWKSAY-----IRQ--HRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primates;
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                                                                                                                                                                                                                                                                                                        21.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ., Harper W., Elledge S.J.;
the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                           92;
                                                                                                                                                                                                                                                                                         Score 640; DB 4;
Pred. No. 4.4e-47;
)2; Mismatches 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                           211; Indels
                                                                                                                                                                                                                                                                                                                     Length 627;
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                                                                                                                                                                                                                                                                                           72;
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                            306
                                                         281
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В
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                                                                                                     Query Match
Best Local
                                                   Matches 167;
                                                                                                                         InterPro; IPR001810; F-box.
InterPro; IPR001880; WD40.
Pfam; pF00646; F-box; 1.
Pfam; pF00400; WD40; 7.
ProDom; PD000018; WD40; 2.
PROSITE; PS50181; FB0X; 1.
PROSITE; PS50181; WD_REPEATS_1; UNKNOWN_5.
PROSITE; PS50284; WD_REPEATS_2; 7.
PROSITE; PS50284; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q969H0;
01-DEC-2001
01-DEC-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=21449048; PubMed=11565034;
C+rohmaier H., Spruck C.H., Kaiser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-UN-2002 (TrEMBLrel. 21, Last annotation
F-box protein CDC4 (Archipelago alpha form).
                                                                                                                                                                                                                                          -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS) EMBL; AY049984; AAL07271.1; -. EMBL; AF411971; AAL06290.1; -.
                                                                                                                                                                                                                                                                                   "Archipelago regulates Cyclin E human cancer cell lines."; Nature 413:311-316(2001).
                                                                                                                                                                                                                                                                                                                                                                            "Human F-box protein hCdc4 targets cyclin mutated in a breast cancer cell line."; Nature 413:316-322(2001).
                                                                                                                                                                                                                                                                                                                        MEDLINE=21449047; PubMed=11565033; Moberg K.H., Bell D.W., Wahrer D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q969н0
                                                                                                     SEQUENCE
                                                                                                               Repeat;
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
  171
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                        14 KFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKT 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSG
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  KLDHGSEVRSFSLGKKPCKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NADSTVKIWDIKTG-------QCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AYDGKIKVWDLVAALDPRAPAGTLCLRTLV---EHSGRVFRLQFDEFQIVSSSHDDTILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QGHTNRVYSLQFDGTHVVSGSLDTSTRVWDVETGNCTHTLTGHQSLTSGMELKDNTLVSG
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                                                               Similarity
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707 AA
                                                   Conservative
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                                                                                                     79663 MW;
                                                            21.18;
                                                92;
                                                                                                                                                                                                                                                                                                                                                                                                                               Kaiser P.,
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Last annotation update)
                                                              Score 640;
Pred. No. 5.
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                                                                                                   E4A357F76DFD8203 CRC64;
                                                   Mismatches
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  -SEYTSTTGL----
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                                                                           DB 4;
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                                                               .2e-47;
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                                                 211;
                                                                        Length 707;
                                                                                                                                                                                                                                                                                                                                                                                                       proteolysis
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                                                   Indels
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RESULT 15
Q8VHP4
ID Q8VHP
AC Q8VHP
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DT 01-MA
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DE F-DOX
GN FBWD66
OS MUS MUS M
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                                  Query Match
Best Local S
         Matches 167;
                                                                                                    PROSITE; PS50181; FBOX; 1.

PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_5.

PROSITE; PS50082; WD_REPEATS_2; 7.

PROSITE; PS50294; WD_REPEATS_REGION; 1.

PROSITE; PS50294; WD_REPEATS_REGION; 1.

PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8VHP4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ilyin G.P.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF427101; AAL50052.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                        SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00320; GPROTEINBRPT. ProDom; PD000018; WD40; 2.
                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00646; F-box; 1
Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FBWD6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F-box protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NADSTVKIWDIKTG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTNWRRGELKSPKV-LKGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGH 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGH 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIERMVRTDSLWRGLAE-----RRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLANGTSSMIVPKORKLSASYEKEKEL--CVKYFEQWSESDQVEFVEHLISQMCHYQHGH 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATLRVWDIETGQCL---HVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWDPETETCLHTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKD 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KCKE-----EGIDEPLHIKRRK-----VIKPGFIHSPWKSAY-----IRQ--HRI 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MMQVIEPQFQRDFISLLP----KELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKK 191
                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             650
         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
21.1%; Score 639; DB 11; 30.8%; Pred. No. 5.4e-47; tive 92; Mismatches 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --QCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKL 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                        Length 629;
   Indels
   72;
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   Gaps
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571 WD 572
                                            544 WD 545
                                                                                  520 NADSTVKIWDIKTG------QCLQTLEGPSKHQSAVTCLQFNKNFVITSSDDGTVKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 INSYLKPMIQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 DINWRRGELKSPKV-LKGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 KLANGTSSMIVFKQRKLSASYEKEKEL--CVKYFEQWSESDQVEFVEHLISQMCHYQHGH 131
                                                                                                                                                                        QGHTNRVYSLQFDGIHVVSGSLDTSIRVMDVETGNCIHTLTGHQSLTSGMELKDNILVSG
                                                                                                                                                                                                                NGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSG 486
                                                                                                                                                                                                                                                                                                                                                                                                 TGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKD 366
                                                                                                                           AYDGKIKVWDLVAALDPRAPAGTLCLRTL---VEHSGRVFRLQFDEFQIVSSSHDDTILI 543
                                                                                                                                                                                                                                                               ATLRVWDIETGQCL---HVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWDPETETCLHTL
                                                                                                                                                                                                                                                                                                          RSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIERMVRTDSLWRGLAE-----RRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MMQVIEPQFQRDFISLLP----KELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWRE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLDHGSEVRSFSLGKKPCKV-----SDYTSTTGL-----VPCSA-----TPTTFGDL 134
                                                                                                                                                                                                                                                                                                                                                       TGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRD 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAANGQG-----QQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKH 189
                                                                                                                                                                                                                                                               459
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Search completed: February 20, 2003, 09:55:19 Job time: 44 secs

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Run on:
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1: /cgn2_6/ptodata/1/pubpaa/U
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9: /cgn2_6/ptodata/1/pubpaa/U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDPAEAVLQEKALKFMNSSE......PAAQAEPPRSPSRTYTYISR 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.3 Coppright (c) 1993 - 2003 Compugen Ltd.
/cgn2_6/ptodata/1/pubpaa/US08_FUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (without alignments)
1038.379 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match I	Length	DB	ID	Description
1	3034	100.0	569	12	US-10-042-417-2	Sequence 2, Appli
2	1163	38.3	219	9	US-10-023-530-2	Sequence 2, Appli
ω	989.5	32.6	265	10	US-09-764-848-30	Sequence 30, Appl
4	644.5	21.2	626	9	US-09-213-888-21	Sequence 21, Appl
υī	644.5		626	9	US-09-328-877A-21	Sequence 21, Appl
6	640	21.1	540	9	US-09-213-888-7	Sequence 7, Appli
7	640	21.1	540	9	US-09-213-888-10	Sequence 10, Appl
œ	640	21.1	540	9	US-09-328-877A-7	Sequence 7, Appli
9	640	21.1	540	9	US-09-328-877A-10	Sequence 10, Appl
10	640	21.1	545	9	US-09-213-888-6	Sequence 6, Appli
11	640	21.1	545	ø	US-09-328-877A-6	Sequence 5, Appli
12	640	21.1	553	9	US-09-213-888-5	Sequence 5, Appli
13	640	21.1	553	9	US-09-328-877A-5	Sequence 5, Appli
14	640	21.1	559	9	US-09-213-888-9	Sequence 9, Appli
15	640	21.1	559	9	US-09-328-877A-9	Sequence 9, Appli
16	640	21.1	589	9	US-09-213-888-8	Sequence 8, Appli
17	640	21.1	589	9	US-09-328-877A-8	α
18	640	21.1	592	9	US-09-213-888-4	Sequence 4, Appli
19	640	21.1	592	9	US-09-328-877A-4	Sequence 4, Appli

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	Ģ O	29	28	27	26	25	24	23	22	21	20
246.5	254.5	260.5	264.5	283	293.5	296.5	299.5	299.5	307.5	316.5	334.5	337	337	384	392	399	455.5	545	575	640	640	640	640	640	640
8.1	8.4	8.6	8.7	9.3	9.7	9.8	9.9	9.9	10.1	10.4	11.0	11.1	11.1	12.7	12.9	13.2	15.0	18.0	19.0	21.1	21.1	21.1	21.1	21.1	21.1
343	316	375	423	713	261	484	1205	1194	742	485	422	1146	1146	732	732	779	1356	640	678	669	669	666	666	627	627
9	10	9	10	10	9	9		10	ø	9		10	9	9	10	9	9	9	10	9	9	9	9	9	9 1
US-10-119-932-5	US-09-828-310-12	US-10-119-932-1	US-09-729-674-160	US-09-801-368-408	US-10-132-744A-4	US-10-132-744A-2	US-09-876-667-16	US-09-876-667-2	US-10-077-111-11	US-10-132-744A-6	US-10-042-417-4	US-09-994-485-6	US-09-832-292-10	US-09-832-292-12	US-09-994-485-8	US-10-060-019-29	US-10-077-111-10	US-10-060-019-30	US-09-801-368-314	US-09-328-877A-25	US-09-213-888-25	US-09-328-877A-27	US-09-213-888-27	US-09-328-877A-3	US-09-213-888-3
sequence o, Appir	Sequence 12, Appr	Sequence I, Appli	sequence Ibu, App	Sequence 408, App	Sequence 4, Appli	Sequence 2, Appli	Sequence 15, Appr	Sequence 2, Appli	Sequence II, Appi	Sequence 6, Appl1	Sequence 4, Appli	Sequence 6, Appli	Sequence 10, Appl	Sequence 12, Appl	Sequence 8, Appli	Sequence 29, Appl	Sequence 10, Appl	Sequence 30, Appl	Sequence 314, App	Sequence 25, Appl	25		2) L	ω

ALIGNMENTS

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; TYPE: PRT ; ORGANISM: Homo sapiens US-10-042-417-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                      Matches 569;
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 3034; DB 12; Length 569; Best Local Similarity 100.0%; Pred. No. 6.5e-248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/042,417
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 60/260,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS FILE REFERENCE: 5914-090-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-01-5
NUMBER OF SEQ ID NOS: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pagano, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 569
                                          181 RYTSDGMLWKKLIERMYRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII 240
                                                                  181 RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII 240
                                                                                                                                  121
                                                                                                                                                  121 ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180
241 QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK 300
                                                                                                                                                                                                                                                        61 STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
                                                                                                                                                                                                              61 STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
                                                                                                                                                                                                                                                                                                ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LEGRAIN, Pierre
APPLICANT: BENAROUS, Richard
APPLICANT: BENAROUS, Richard
APPLICANT: BLOT, Guillaume
APPLICANT: LASSOT, Irina
TITLE OF INVENTION: PROTEINS THAT INTERACT WITH BETA TICP
FILE REFERENCE: B4717A
CURRENT APPLICATION NUMBER: US/10/023,530
CURRENT FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/256,276
PRIOR APPLICATION NUMBER: 60/256,276
PRIOR FILING DATE: 2000-12-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: BetaTrCP
LOCATION: (1)..(219)
OTHER INFORMATION: F-box protein
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                               181 RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKN 219
                                                                                       181 RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKN 219
                                                                                                                                                 121 ISOMCHYOHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180
                                                                                                                                                                                                            61 STANKTENCVAKTKLANGTSSMIVFKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
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                                                                                                                                                                                                                                                                                          1 MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60
                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                            ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180
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                                                                                                                                                                                                                                                                                                                                                                                        219; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219
                                                                                                                                                                                                                                                                                                                                                                                                 38.3%; Score 1163; DB 9; Length 219; 100.0%; Pred. No. 9.6e-91;
                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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US-09-213-888-21
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; Sequence 30, Application US/09764848
; Patent No. US20020077270A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-848-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prior application data removed - consult PALM or file wrapper; NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
SEQ ID NO 30
                                                                                                                                                                                                                                        SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21, Application US/09213888A Patent No. US20020164683A1
                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
             Matches 169;
                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/213,888A CURRENT FILING DATE: 1998-12-17 NUMBER OF SEQ ID NOS: 27 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gurney, Mark E. APPLICANT: Li, Jinhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 6142
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT208
CURRENT APPLICATION NUMBER: US/09/764,848
CURRENT FILING DATE: 2001-01-17
                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: homo sapien
                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                     FEATURE:
                                                                                                                                                                                              LENGTH: 626
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 RMVRTDPLWKGLSERRGWDQYLFKNRPTDG--PPNSFYRSLYPKIIQDIETIESNWRCGR
                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 HNLQRIQCRSENSKGVYCLQYDDEKIISGL 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 YLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 YLKPMLQRDFITALPEQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLIE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 ISNGTSSVIVSRKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHINS 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 LANGTSSMIVPKORKLSASYEKEKELCVKYFEOWSESDQVEFVEHLISOMCHYOHGHINS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 FQNTSVMEDQNEDESPK-----KNTLWQ------
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      Conservative 103; Mismatches
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                     21.2%; Score 644.5; DB 9; 30.1%; Pred. No. 2.1e-46;
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  222;
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                                         Length 626;
Indels 67;
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Gaps
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8 LQEKALKFMNSSEREDCNNGEPPRKIIPEK--NSLRQ--TYNSCARLCLNQETVCLASTA 63

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                                                                                                                                                     US-09-328-877A-21
                                                                                                                                                                                                                                                                                      SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/09328877A Patent No. US20020177187A1
                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/328,877A CURRENT FILING DATE: 1999-06-09 NUMBER OF SEQ ID NOS: 27 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gurney, Mark E. APPLICANT: Li, Jinhe
                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: homo sapien
                                                                                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  525 LQFDEFQIVSSSHDDTILIWD 545
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53
                                  8
                                                                                            Joca 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WKSAY-----IRQ--HRIDTNWRRGELKSPKV-LKGHDDHVITCLQFCGNRIVSGSDDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAE-----RRGWGQYLFKNKPPDGNAP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEQKLISEEDLNEMESLGDLTMEQKLISEEDLNSMKRKLDHGSEVRSFSLGKKPCKVSEY 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAVLHLRFNNGMMYTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKTENCV-----AKTKLANGTSSMIVPKQRKLSASYEKEKEL--CVKYFEQWSESD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GHQSLTSGMELKDNILVSGNADSTVKIWDIKTG-----QCLQTLQGPNKHQSAVTC 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLE
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                                  LQEKALKFMNSSEREDCNNGEPPRKIIPEK -- NSLRQ -- TYNSCARLCLNQETVCLASTA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQFNKNFVITSSDDGTVKLWD 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YDFMYKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLT
MEQKLISEEDLNEMESLGDLTMEQKLISEEDLNSMKRKLDHGSEVRSFSLGKKPCKVSEY 112
                                                                          169;
                                                                                                                                                                                                                                                                      626
                                                                                            Similarity
                                                                        Conservative
                                                                                          21.2%; Score 644.5; DB 9; 30.1%; Pred. No. 2.1e-46;
                                                                        103;
                                                                        Mismatches
                                                                        222;
                                                                                                             Length 626;
                                                                        Indels
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                                                           Вb
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                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09213888A Patent No. US20020164683A1
                                                                                                                                                                                                                     Matches 167;
                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/213,888A CURRENT FILING DATE: 1998-12-17 NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                            LENGTH: 54
TYPE: PRT
                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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                   132 INSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKK 191
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                                                             46
                                                                                                 74
                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                             14 KFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQTCRYWRILAEDNLLWREKCKE-----EGIDEPLHIKRRK-----VIKPGFIHSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLV---EHSGRVFR 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHT 380
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                                                         RAANGQG-----QQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKH 100
                                                                                             KLANGTSSMIVPKORKLSASYEKEKEL--CVKYFEQWSESDQVEFVEHLISQMCHYQHGH 131
                                                                                                                                         KLDHGSEVRSFSLGKKPCKV-----SEYTSTTGL-----VPCSA-----TPTTFGDL 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOFDEFOIVSSSHDDTILIWD 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STVRCMHLHEKRVVSGSRDATLRVWDIETGQCL---HVLMGHVAAVRCVQYDGRRVVSGA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSAS 407
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                                                                                                                                                                                                                                                                                                                                                                 540
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30.8%; Pred. No. 4.1e-46;
ative 92; Mismatches 211;
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                                                                                                                                                                                                                                                             Length 540;
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                       72;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
US-09-328-877A-7
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Patent No. US20020177187A1

GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENUM APPLICANT ON THE PROPERTY OF THE PROP
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307 TGSVLCLQYDERVIITGSSDSTYRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKD 366
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CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
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APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele i
APPLICANT: Pharmacia 6 Up
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ORGANISM: Homo sapiens
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367 RSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTL 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 21.1%; Score 640; DB 9; Length 540; Local Similarity 30.8%; Pred. No. 4.1e-46; es 167; Conservative 92; Mismatches 211; Indels 72;
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                                                                                                                               TGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKD 366
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APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
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LENGTH: 545
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                                                                376 QGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSG
                                                                                                              427 NGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSG 486
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                 487 AYDGKIKVWDLVAALDPRAPAGTLCLRTLV---EHSGRVFRLQFDEFQIVSSSHDDTILI 543
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; TYPE: PRT ; ORGANISM: Homo sapiens US-09-328-877A-6
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GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
APPLICANT: Pharmacia & Upjohn Company
TNUENTION: Human Sel-10 Polypeptides and Polynucleotides that
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LENGTH: 545
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; GENERAL INFORMATION;
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                      Sequence 5, Application US/09328877A Patent No. US20020177187A1
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CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 553
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US-09-213-888-5
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APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
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ORGANISM: Homo sapiens
495 WD 496
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                                                                         444 NADSTVKIWDIKTG------QCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKL
                                                                                                                     487 AYDGKIKVWDLVAALDPRAPAGTLCLRTLV---EHSGRVFRLQFDEFQIVSSSHDDTILI 543
                                                                                                                                                                    384 QGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSG
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                                                                                                                  Sequence 9, Application US/09213888A Patent No. US20020164683A1 GENERAL INFORMATION:
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SEQ ID NO 5
LENGTH: 553
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jihhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
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APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polype
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
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CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-9
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CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
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Best Local :
SOFTWARE:
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                                                                                                                                            APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele
APPLICANT: Pharmacia & Up
                                 CURRENT APPLICATION NUMBER: US/09/328,877A CURRENT FILING DATE: 1999-06-09 NUMBER OF SEQ ID NOS: 27
                                                                                         TITLE OF INVENTION: Human TITLE OF INVENTION: Encoderile Reference: 6142
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Local Similarity 30.8%; Pred. No. 4.3e-46;
nes 167; Conservative 92; Mismatches 211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAANGQG-----QQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLDHGSEVRSFSLGKKPCKV-----SEYTSTTGL-----VPCSA-----TPTTFGDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKD
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                                                                                                                  487 AYDGKIKVWDLVAALDPRAPAGTLCLRTLV---EHSGRVFRLQFDEFQIVSSSHDDTILI 543
                                                                                                                                                             390 QGHTNRVYSLQFDGIHVVSGSLDTSIRVMDVETGNCIHTLTGHQSLTSGMELKDNILVSG
                                                                                                                                                                                                                                                                         367 RSTAVWDMASPTDITLRRVLVGHRAAVNVVDEDDKYIVSASGDRTIKVWNTSTCEEVRTL 426
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                                                                            450 NADSTVKIWDIKTG------QCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKL 500
                                                                                                                                                                                                     427 NGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSG 486
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                                                                                                                                                                                                                                                                                                                                  273
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Search completed: February 20, 2003, 10:00:10 Job time : 17 secs

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	Segmence 50571.	Sequence 3221, A	Sequence 3221, Ap	Sequence 4, Appl	Sequence 2, Appl.	Sequence 4360, Ap	Sequence 150, App	Sequence 112, App	Sequence 144, App	Sequence 2768, Ap	Sequence 114, App	•	Sequence 116, App	•	Sequence 60984, 1	Sequence 60984, 2	Sequence 61379, A	Sequence 61378, 2	Sequence 61377, 1

Application US/09601168B

APPLICANT:

APPLICANT: APPLICANT: RESULT 1

ALIGNMENTS

US-09-601-168B-2

Sequence 2, Applicat GENERAL INFORMATION:

APPLICANT: BENAROUS, Richard

; OTHER INFORMATION: Description of the artificial sequence : OTHER INFORMATION: coding for human beta-TrCP protein US-09-601-168B-2 NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver: 2.1 and manually
SEQ ID NO 2
LENGTH: 569 Query Match
Best Local Similarity PRIOR APPLICATION NUMBER: PCT/FR99/00196
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: FR98 01100
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: FR98 15545
PRIOR FILING DATE: 1998-12-09 APPLICANT: MARGOTTIN, Florence APPLICANT: DURAND, Herve FILE REFERENCE: 935.38812X00
CURRENT APPLICATION NUMBER: US/09/601,168B
CURRENT FILING DATE: 2000-07-28 TITLE OF INVENTION: Human beta-TrCP protein ORGANISM: Artificial sequence 181 RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII 240 61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKYFEOMSESDOVEFVEHL 120 1 MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60 1 MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60 STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120 569; KROLL, Mathias CONDORCET, Jean-Paul ARENZANA SEISDEDOS, Fernando Conservative 100.0%; Score 3034; DB 5; 100.0%; Pred. No. 5e-273; ative 0; Mismatches 0; Indels Length 569; CDNA 0; Gaps

TYPE: PRT FEATURE:

Вb

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Matches

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181

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CURRENT APPLICATION NUMBER: US/99/
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 52731
LENGTH: 605
TYPE: PRT
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19-724-676-52731
325 SDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRR
                                         301 ETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGS
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94.0%;
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 52731
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
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TYPE: PRT
      421 VLVGHRAAVNVVDFDDKYIVSASGDRIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVV
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                                                                                         SDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRR 420
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Similarity 94.08;
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 Mismatches

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Pred. No. 2.2e-270;
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT EILING NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
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TYPE: PRT
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                                                                                 KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT 540
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                                                                                                                                                                                                VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
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LENGTH: 537
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Local Similarity 91.2%;
                                                                                                                      541 ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
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; Sequence 52729, Application US/09724676A ; GENERAL INFORMATION:

APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION NUMBER: US/09/724,676A CURRENT FILING DATE: 2000-11-28

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RESULT 7
US-09-724-676A-52730
; Sequence 52730, App
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; ORGANISM: Homo sapiens
US-09-724-676A-52729
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 52730
LENGTH: 537
            Matches 519;
                                               Query Match
                                                                                                                                                                                                                                                                                      GENERAL INFORMATION
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Best Local Similarity
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SEQ ID NO 52729
LENGTH: 537
                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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                           Similarity
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                    89.0%; Score 2701; DB 5; 91.2%; Pred. No. 3.8e-242;
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                                    DB 5; Length 537;
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; GENERAL INFORMATION:
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LENGTH: 573
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Best Local Similarity
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEO ID NOS: 97222
SOFTWARE: Patentin version 3.2
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
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                                                    541 ILIMDFLNDPAAQAEPPRSPSRTYTYISR 569
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                                                                                                                                                                                                                88.1%; Score 2673; DB 5; Length 573; 85.8%; Pred. No. 1.7e-239;
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LENGTH: 573
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 52732
LENGTH: 573
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity 85.8%;
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
FILE REFERENCE: 129181.4 Compugen
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
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                                                                                           SDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRR 384
                                                                                                                                                               ETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGS
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                                                                       SDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRR
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 61015
LENGTH: 529
TYPE: PRT
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                                                                     KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT 540
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                                                  KRIVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDT
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43; Mismatches
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 61016
LENGTH: 529
TYPE: PRT
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                                                                  Sequence 61015, Application US/09724676A GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER:
             APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen
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                                                                                                                                                                                                   ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
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US/09/724,676A
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                                                                                             ; ORGANISM: Homo sapiens US-09-724-676A-61016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-724-676A-61016
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; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo s
                                                                                                                                                                                    APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 61016
LENGTH: 529
TYPE: THE SECTION OF THE SECTIO
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Local Similarity 79.3%; Pred. No. 3.3e-214;
43: Mismatches 35;
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ID NOS: 97222
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79.1%;
   Score
Pred.
   2400; DB 5;
No. 3.3e-214;
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Matche	Matches 451; Conservative 43; Mismatches 35; Indels 40; Gaps 4	
Qу	1 MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETYCLA 60	
Db	1 MEP-DSVIEDKTIELMNTSVMEDQNEDESPKKNTLWQ 36	
Qy (£S.≵	
Db	37ISNGTSSVIVSRKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHL 82	
Qy 121		
Db	83 ISRMCHYQHGHINSYLKPMLQRDFITALPEQGLDHIAENILSYLDARSLCAAELVCKEWQ 142	
Qy 181		
Db 143	43 RVISEGMIWKKLIERMYRTDPIWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKII 200	
Qy 241	_	
Db 201	01 QDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISGLRDNSIKIWDKTSLECL 260	
Qy 301		
Db 261	61 KVLTGHTGSVLCLQYDERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLM 320	
Qу 361		
Db 321	21 VTCSKDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWSTSTC 380	
Qy 421		
Db 381	81 EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN 440	
Qy 481		
Db 441	41 KRIVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDT 500	
Qy 541	ILIWDFLNDPAAQAEPPI	
Db 501	01 ILIWDELNVPPSAQNETRSPSRTYTYISR 529	

Search completed: February 20, 2003, 09:59:48 Job time: 59 secs

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3034	303 4 303 4	3034	3034	3034	Score
100.0	100.0	100.0	100.0	100.0	Query Match
569	569 569	569	569	569	Query Match Length DB
18	17	16	_	Н	DB
US-09-455-371-2	7 US-09-385-219-2 B US-09-415-795-4	US-09-210-060-18	PCT-US99-19560-2	PCT-US02-00311-2	ID
Sequence 2, Appli	Sequence 2, Appli	Sequence 18, Appl	Sequence 2, Appli	Sequence 2, Appli	Description

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Sequence 27, Appl Sequence 6384, Ap	12736	121061	e 6363, A	e 368	12	25894,	e 6925	9	16,	11197,	3353	e 16, A	1789,	e 368	30, 2	26, A	e 83876	1245, A	e 12963	3214,		3212, Ap	e 21214,	1246, A	131810	12, App	e 228	_	2	5	2	8,	e 18, A	e 8016	e 12,	e 2, Ap	Sequence 2, Appli

ALIGNMENTS

RESULT 1 PCT-US02-00311-2

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Sequence 2, Application PC/TUS0200311

SERVERAL INFORMATION:
APPLICANT: Pagano, M.
APPLICANT: Pagano, M.
TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF TITLE OF INVENTION: PROLIFERATIVE AND DIFFERNTIATIVE DISORDERS
FILE REFERENCE: 5914-090-228
CURRENT APPLICATION NUMBER: PCT/US02/00311
CURRENT FILING DATE: 2002-01-07
PRIOR FILING DATE: 2001-01-5
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 2
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 569
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-00311-2

Query Match
Best Local Similarity 100.0%; Score 3034; DB 1; Length 569;
Best Local Similarity 100.0%; Pred. No. 1.3e-284;
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: NEW YORK UNIVERSITY
TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
FILE REFERENCE: 5914-081-228
CURRENT APPLICATION NUMBER: PCT/US99/19560
CURRENT FILING DATE: 1999-08-31
EARLIER FILING DATE: 1998-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 89 SOFTWARE: PatentIn Ver. 2.0
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EARLIER FILING DATE: 1999-03-15
                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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121 ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180
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                                                                                   61 STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
                                                           61 STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
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                                                                                                                                         MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60
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SEQ ID NO 18
LENGTH: 569
TYPE: PRT
ORGANISM: Homo sapiens
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; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION TITLE OF INVENTION: NF-kB FILE REFERENCE: 860098.427
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APPLICANT: Mercurio, Frank
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APPLICANT: Yaron, Avraham
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181 RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII 240
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                                                          121 ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180
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Davis, Matti
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS FILE REFERENCE: 5914-081
CURRENT APPLICATION NUMBER: US/09/385,219
CURRENT FILING DATE: 1999-08-27
EARLIER APPLICATION NUMBER: 60/098,355
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: 60/118,568
EARLIER FILING DATE: 1999-02-03
EARLIER APPLICATION NUMBER: 60/124,449
EARLIER FILING DATE: 1999-03-15
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin Ver. 2.0
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    Application US/09385219

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US-09-415-795-4
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APPLICANT: HowLey, Peter M.
APPLICANT: HowLey, Peter M.
TITLE OF INVENTION: TARGETED PROTEOLYSIS BY
TITLE OF INVENTION: PROTEIN LICASES
FILE REFERENCE: HMV-043.01
CURRENT APPLICATION NUMBER: US/09/415,795
CURRENT FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 47
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SEQ ID NO 4
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Pred. No. 1.3e-284;
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US-09-455-371-2
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APPLICANT: Winston, Jeffrey T.
APPLICANT: Winston, Jeffrey T.
TITLE OF INVENTION: Regulation of I Kappa B (IK-B) Degradation and Methods and Reagen
TITLE OF INVENTION: Related Thereto
FILE REPERENCE: 120541-1010
CURRENT EPPLICATION NUMBER: US/09/455,371
CURRENT FILING DATE: 1999-12-03
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APPLICANT: Elledge, Stephen
APPLICANT: Harper, J. Wade
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GENERAL INFORMATION:
Beer-Romero, Peggy
APPLICANT: Beer-Romero, Peggy
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SEQ ID NO 2
LENGTH: 569
TYPE: PRT
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TITLE OF INVENTION: Regulation of I Kappa B (IK-B) Degradation and Methods and Rea
TITLE OF INVENTION: Related Thereto
FILE REFERENCE: 120541-1010
CURRENT APPLICATION NUMBER: US/09/455,371B
CURRENT FILING DATE: 1999-12-03
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PRIOR APPLICATION NUMBER: PCT/FR99/00196
PRIOR ETLING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: FR98 01100
PRIOR FILING DATE: 1998-01-30
PRIOR FILING DATE: 1998-12-09
PRIOR FILING DATE: 1998-12-09
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TYPE: PRT
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VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC 420
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CURRENT FILING DATE: 2002-08-26

PRIOR APPLICATION NUMBER: 60/085,3434; 60/098,010

PRIOR FILING DATE: 1998-05-13; 1998-08-26
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TITLE OF INVENTION: CELL SIGNALING PROTEINS
FILE REFERENCE: PF-0521 PCT
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ORGANISM: Homo sapiens
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NAME/KEY: misc-feature
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361 VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC
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; ORGANISM: Homo sapiens US-09-791-537-80169
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LENGTH: 569
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APPLICANT: Dobe, Derek
APPLICATION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
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    Mismatches

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SOFTWARE: PatentIn Ver. SEQ ID NO 18
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GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/210,060
PRIOR FILING DATE: 1998-12-10
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APPLICANT: Mercurio, Frank
APPLICANT: Amit, Sharon
APPLICANT: Ben-Neriah, Yinon
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481 KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT 540
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Yaron, Avraham
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Hatzubai, Ada
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US-10-038-010-8
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APPLICANT: Pierre, Legrain
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
FILE REFERENCE: B4767A
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TYPE: PRT
ORGANISM: Homo sapiens
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LOCATION: (1)..(569)
OTHER INFORMATION:
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541 ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
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ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
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Sequence 2, Application US/10042417
; GENERAL INFORMATION:
; APPLICANT: PAGANO, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE
; TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
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Best Local
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TYPE: PRT
ORGANISM: Homo:
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US-60-098-010-5; Sequence 5, Applicati; GENERAL INFORMATION: APPLICANT: Yue, Hen

Yue, Henry Application

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                                                 Sequence 2, Application US/60098355
GENERAL INFORMATION:
APPLICANT: Chiaur, Dah Shiarn
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LENGTH: 569
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 APPLICANT: Pagano, NAPPLICANT: Latres, FITTLE OF INVENTION:
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CURRENT FILING DATE: 1998-08-26
NUMBER OF SEQ ID NOS: 12
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APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: G-PROTEIN SIGNALING PATHWAY MOLECULES
FILE REFERENCE: PF-0583 P
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APPLICANT: Lal, Preeti
APPLICANT: Baughn, Mari
APPLICANT: Patterson, (
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US-60-098-355-2
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CURRENT FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 2
LENGTH: 569
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length DB	ength		ID	Description
1	3034	100.0	569	20	AAY24054	A human beta-trans
2	3034	100.0	569	21	AAB12813	Human beta-transdu
ω	3034	100.0	569	21	AAY96697	Human beta-TrCP.
4	3034	100.0	569	21	AAY83041	F-box protein FBP-
տ	3034	100.0	569	21	AAY83250	F-box protein hBet
σ	3034	100.0	569	21	AAY44249	Human cell signall
7	3027	99.8	569	22	AAB48298	Human ZFll protein
6 0	3027	99.8	809	22	AAM00960	Human bone marrow
9	3006	99.1	605	22	AAM78582	Human protein SEQ
10	2997	98.8	569	21	AAB12812	Mouse ubiquitin li

4	4	4	٠		4	ω	ω	ω	ω	w	ω	ω	ω	ω	w	2	2	2	2	2	2	2	2	N	N	<u>.</u>		٠,	Ľ	<u>::</u>	_		12	н,
Ŭτ														_	_							2	2	N	N	2	2			29	25	29	29	
640				640					640				0	Çī	u				935		ω	G	UI	Ğ	ū	G	'n							97
21.1	21.1	•	•	٠	21.1	21.1	21.1	21.1	21.1	21.1	21.1	21.1	21.1	21.2	21.2	21.8	21.8	21.8	30.8	32.6	38.3	68.9	78.6	78.6	78.6	78.6	85.1	95.0	97.6	98.5	98.5	98.5	98.6	98.8
589	589	589	559	559	553	553	553	545	545	540	540	540	540	626	626	1326	1326	1326	448	265	219	510	550	542	542	542	517	579	590	654	654	654	632	569
22	21	20	22	20	22	22	20	22	20	22	22	20	20	22	20	22	22	22	22	22	23	22	22	22	22	21	16	22	22	22	22	22		21
AAB59198	AAB01204	AAY22466	AAB59199	AAY22467	AAB59195	AAB93475	AAY22463	AAB59196	AAY22464	AAB59200	AAB59197	AAY22468	AAY22465	AAB59201	AAY22469	ABB70051	ABB67238	ABB67237	AAB48289	AAU86942	AAU98087	ABB59857	AAM41994	AAM40208	AAM79127	AAY96696	AAR85852	AAM78583	AAM00847	AAM79568	AAM79567	AAM79566	AAM78584	AAY83254
Human mammary sel-	Human GTPase assoc	Human mammary sel-	Human mammary sel-		Human hippocampal	Human protein sequ	Human hippocampal	Human hippocampal	Human hippocampal	Human mammary sel-	Human hippocampal	Human mammary sel-	Human hippocampai	Protein encoded by	Human 6myc-N-sel-1	melano				Human DNA repair a	Human beta TrCP (b	Drosophila melanog	Human polypeptide	Human polypeptide	Human protein SEQ	Human E3 ubiquitin	WD-40 domain-contg		Human bone marrow	Human protein SEQ				

ALIGNMENTS

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AAY24054; AAY24054 standard; Protein; 569 AA. 30-SEP-1999 (first entry)

A human beta-transducin repeat containing protein.

Beta-transducin repeat containing protein; beta-TrcP; Skplp; proteosome degradation pathway; Vpu protein; beta-Gatenin; human immune deficiency virus-1; HIV-1; cellular protein; IKappaB; ubiquitinylation; phosphorylated protein; tumour; apoptosis; Alzheimer's; antiviral; antitumour; cell cycle regulation; protein degradation; and anti-inflammatory; osteo-articular inflammation; acute inflammation; tumour necrosis factor

Homo sapiens.

Region	Region	Region	Region	Region	Key Region
427455 /note= "WD motif"		/note= "WD motif"	700te= "WD motif"	/HOLE- r DOX sequence 259292 /notes "WD motif"	Location/Qualifiers 147191

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The present sequence represents a human beta-transducin repeat containing C protein (beta-TrcP). The protein directs proteins to the proteosome CC degradation pathways. The protein is able to interact with the Vpu CC protein of human immune deficiency virus-1 (HIV-1), cellular proteins CC likappaB or beta-catenin (bC) and/or protein Skplp. The protein controls CC ubiquitinylation of phosphorylated proteins and thus their targeting to CC proteosomes for degradation. Depending on whether the process is CC inhibited or promoted, the result may be delayed breakdown of CD4 (in CC cases of HIV-1 infection); increased activity of IkB (and thus reduced CC activity of NFkappaB) and increased activity of mutant bC in tumour CC cells, or increased bC survival (and reduced apoptosis) in Alzheimer's CC nucleic acid, are used to screen for anti HIV-1 agents (antivirals), CC antitumour agents that disrupt cell cycle regulation or protein CC disrupt activation by NFkappaB. Fragments of the protein are also CC useful for treating osteo-articular inflammation or acute inflammation
                                                                                                                                                                                                                                                                                                                                                                          Matches 569;
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            associated with release of tumour necrosis factor.
241 QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK
                 241 QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQVDDQKIVSGLRDNTIKIWDKNTLECK 300
                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 60-61; 71pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-inflammatory and anti-Alzheimer's agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human beta-transducin repeat containing protein and its fragments useful as, or to screen for, antiviral, antitumour,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX86501
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30-JAN-1998;
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                                                                    RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII
                                                                                                       RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII 240
                                                                                                                                                                                                                STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
                                                                                                                                                                                                                                       STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKYFEOWSESDOVEFVEHL 120
                                                                                                                                         ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180
                                                                                                                                                                           ISQMCHYQHGHINSYLKDMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180
                                                                                                                                                                                                                                                                                        MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETYCLA
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                                                                                                                                                                                                                                                                                                                                                                       Conservative
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98FR-0001100.
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Pred. No. 1.4e-286;
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Query Match Best Local Similarity

Conservative

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100.0%;

100.0%; Score 3034; DB 21; 100.0%; Pred. No. 1.4e-286;

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                        The present invention describes an F-box motif protein of ubiquitin ligase SCF complex which promotes the ubiquitination of IkappaB or beta-catenin and is constituted by Skpl protein, Cull protein and a complex (SCF complex) of F-box protein containing F-box motif and WD40 repeat motif and has the amino acid sequence of 45 residues (AAB12811) or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin ligase FWD1 protein) and (AAB12B13, which is human beta-transducin repeat containing protein (beta-TrCP)). The F-box protein can be used for the gene therapy of colon cancer by being recombined to a virus vector.
Sequence
                                                                                                                                                                                                            Claim 3; Page 10-12; 19pp; Japanese.
                                                                                                                                                                                                                                            F\text{-}box\ protein of ubiquitin ligase SCF complex which promotes the ubiquitination of <code>IKappaB</code> or beta-catenin -
                                                                                                                                                                                                                                                                                                              N-PSDB; AAA73132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ubiquitin ligase SCF complex; F-box protein; ubiquitination; IkappaB; beta-catenin; Skpl; Cull; F-box motif; WD40 repeat motif; FWD1; gene _therapy; colon cancer; beta-transducin repeat containing protein;
                                                                                                                                                                                                                                                                                                                              WPI; 2000-485550/43
                                                                                                                                                                                                                                                                                                                                                                                                                                      02-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human beta-transducin repeat containing protein (beta-TrCP) SEQ ID NO:3
                                                                                                                                                                                                                                                                                                                                                            (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUN-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  beta-TrCP
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WPI; 2000-431294/37
N-PSDB; AAA51229.
                                                                                                                          (SIGN-)
                                                                                                                                                                                                                                                                             15-JUN-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY96697 standard; Protein;
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Polypeptide enhancing phosphorylated lkappaB ubiquitination treating disorder associated with NF-kappaB activation e.g. comprising amino acid sequence of human E3 ubiquitin ligase
                                                                                                                                   or its
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Claim 21; Page 72-74; 77pp; English.

Human beta-TrCP, an F-box/WD protein family member, has been shown to Chave homology to human E3 ubiquitin ligase (E3). E3 enhances ubiquitination of phosphorylated I-kappa-B, an inhibitor protein of C2 ubiquitination of phosphorylated I-kappa-B. In inhibitor protein of nuclear factor kappa-B (NF-kappa-B). Understanding I-kappa-B C2 degradation via the ubiquitin pathway is useful for identifying C3 modulators of this process for use in treating diseases associated with C4 activation of NF-kappa-B. In vitro analysis suggests that deletion of C4 the F-box results in a protein that functions as a dominant negative molecule in vivo. Translent over-expression of delta-beta-TrCP (a deletion mutant) inhibited the degradation of endogenous I-kappa-B-alpha C3 can be used to screen for modulators of NF-kappa-B CC in stimulated Jurkat cells, resulting in accumulation of phosphorylated C1 -kappa-B-alpha B can be used to screen for modulators of NF-kappa-B CC inflammatory diseases, autoimmune diseases, cancer and viral infections. Sequence 569 AA;

Similarity 100.0%; Score 3034; DB 21; ilarity 100.0%; Pred. No. 1.4e-286; Conservative 0; Mismatches 0; Indels Length

Query Match Best Local S Matches 569 0; 0

Дb Ş 밁 Qy 61 61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKYFEOWSESDOVEFVEHL 120 MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 60

ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY

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Q 421 EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acid for screening compounds useful for treating proliferative and differentiative disorders such as cancer and disorders comprises sequences encoding ubiquitin limages.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Figure 3a; 245pp; English.
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03-FEB-1999;
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              RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII
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N-PSDB; AAZ93710.
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The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin ligases) which can be used for the targetted degradation of a target polypeptide in vivo. Targetted degradation is achieved by expressing the ubiquitin ligase in a cell linked to the interaction domain of the target polypeptide and thereby recruiting the target polypeptide to the ubiquitin ligase. Such methods are useful for decreasing or increasing the level of a target polypeptide and for creating and expressing a destabilized polypeptide which is subjected to SCF mediated proteolysis. Degrading any desired protein in a cell is

Claim 9; Page 171; 185pp; English.

Modified-site

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                                                         Cell signalling protein-12; CSIGP-12; cell proliferation; inflammatory disorder; cirrhosis; cancer; hepatitis; AIDS arteriosclerosis; Addison's disease; multiple sclerosis.
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59; Conservative
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Pred. No. 1.4e-286;
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Human cell signaling proteins useful for, proliferative and inflammatory disorders

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Best Local
                  Human ZF11 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressed in musculoskeletal, gastrointestinal and nervous tissues and is found to be homologous to beta-transducin repeats containing protein. Fragments of CSIGP encoding nucleic acid can be used as hybridisation probe for detecting CSIGP related sequences or allelic variants. Recombinant CSIGP can be produced in host cells by transforming them with genetically engineered vectors. Agonists or antagonists can be used in the treatment of cell proliferative and inflammatory disorders associated with decreased or increased CSIGP expression. CSIGP is used in the diagnosis, prevention and treatment of cell proliferative disorders like arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory
                                                     02-APR-2001
                                                                                                                           AAB48298 standard;
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Pred. No. 1.4e-286;
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EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN

VTCSKDRSIAVWDWASFTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC

RILTGHTGSVLCLQYDGRVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMM

VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC

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                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to methods of altering the polypeptide levels in a cell, using proteins selected from S-phase kinase associated proteins 1 and 2 (SRP1, SRP2), SRP2-like proteins (ZF) and CUL-1 (a member of the cullin/ CDC53 family of proteins). The method is useful for altering the level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2 polypeptide in a cell. SRP2 and SRP2-like protein levels are useful for detecting tumours, and in monitoring tumor treatment in a mammal. Agents that modulate interactions between SKP and target proteins are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 130-132; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modulating polypeptide levels in a cell, diagnosing and treating tumor, involves altering levels of proteins such as S-phase kinase associated proteins 1, 2 and cullin/CDC53 proteins -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAC84610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S-phase kinase associated protein; SKP1; SKP2; CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-2000; 2000WO-US15449
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                   301
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                                                                                                                                                                                                                                                                            61 STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
                                                                                                                                                                                                                                                                                                                                           1 MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60
                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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RILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMM
                                                QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK
                                                                    QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK 300
                                                                                                                    RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII
                                                                                                                                      RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII 240
                                                                                                                                                                                     ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY
                                                                                                                                                                                                                      ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180
                                                                                                                                                                                                                                                      STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                569 AA;
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21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
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         be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of chemical compounds as potential drugs.
                                                                                                                                                                                                                                                                                                                                                        Ford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
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                                                                                                                                                                            The present sequence is one of 251 novel human polypeptides encoded by a bone marrow-expressed polynucleotide. The polynucleotide and the
                                                                                                                                                                                                                    Claim 10;
                                                                                                                                                                                                                                            Zhao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM00960;
                                                                                                                                                 polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may
                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-)
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)B; AAH90079.
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lang J, Wer
Zhou P, I
                                                                                                                                                                                                                    Page 523-524; 648pp; English.
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2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
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2000US-0552317
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Werhman T, Xu C,
, Drmanac RT;
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03-FEB-2000;
27-APR-2000;
20-JUN-2000;
                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                    AAM78582
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                                                                                                                                                                                                                                   Human protein SEQ ID NO 1244.
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                                                      05-FEB-2001;
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                                                                                                            WO200157190-A2
                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT
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; 2000US-0496914.
; 2000US-0560875.
; 2000US-0598075.
                                                      2001WO-US04098
                                                                                                                                                                                                                                                                                                                     Protein;
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01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activinyinhibin activity and may be useful in the diagnosis and/or reatment of cancer lenvisories are constant at the diagnosis and/or reatment of cancer lenvisories.
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Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; Page 3503-3504; 6221pp; English.
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        421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      were missing at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AAM80020) are omitted as the relevant pages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment of cancer, leukaemia, nervous system disorders, arthritis and
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VLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVV
                                                                SDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMAVTCSKDRSIAVWDMASPTDITLRR
                                                                                SDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRR 384
                                                                                                                            ETSKGYYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGS
                                                                                                                                                          ETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGS
                                                                                                                                                                                       GLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRS
                                                                                                                                                                                                           GLAERRGWGQYLEKNKPPDGNAPPNSEYRALYPKIIQDIETIESNWRCGRHSLQRIHCRS
                                                                                                                                                                                                                                                                                                                                     PKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDF 144
                                                                                                                                                                                                                                                                                                                                                                            NNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTKLANGTSSMIV 120
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                                                                                                                                                                                                                                                      ITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWR
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                                                                                                                                                                                                                                                                                                                  PKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDF
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Wang D, Wang J, Zhang J, Ren
Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       605 AA;
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; 2000US-0654936.
; 2000US-0663561.
; 2000US-0693325.
; 2000US-0728422.
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94.0%;
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Frad. No. 8.5e-284;
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MDPAEAVLQEKALKEMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCINQETVCLT 60 STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120

121 ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180

STAMKTENCVAKAKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL

Matches

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Conservative

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               Query Match
                                                               The present invention describes an F-box motif protein of ubiquitin ligase SCF complex which promotes the ubiquitination of IkappaB or beta-catenin and is constituted by Skpl protein, Cull protein and a complex (SCF complex) of F-box protein containing F-box motif and wp40 repeat motif and has the amino acid sequence of 45 residues (AAB12811) or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin ligase FWD1 protein) and (AAB12813, which is human beta-transducin repeat containing protein (beta-TrCP)). The F-box protein can be used for the gene therapy of colon cancer by being recombined to a virus vector.
                                                                                                                                                                                                                                             F-box protein of ubiquitin ligase SCF complex which promotes the ubiquitination of IkappaB or beta-catenin -
                                              Sequence
                                                                                                                                                                                                                        Claim 2; Page 9-10;
                                                                                                                                                                                                                                                                                                             WPI; 2000-485550/43.
                                                                                                                                                                                                                                                                                                                                                                        02-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ubiquitin ligase SCF complex; F-box protein; ubiquitination; IkappaB; beta-catenin; Skpl; Cull; F-box motif; WD40 repeat motif; FWD1; gene therapy; colon cancer; beta-transducin repeat containing protein;
                                                                                                                                                                                                                                                                                                                                           (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus.
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                                                                                                                                                                                                                                                                                               AAA73131.
                                           569 AA;
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98.8%;
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Score 2997; DB 21; Pred. No. 5.8e-283;
          Length 569;
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                                                                                                                                                                                                     09-0CT-1998;
                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                   destabilisation; proteolysis; drug discovery; gene therapy; cancer; oncoprotein; Huntington's disease; gene knockout; delivery systems;
                                                                                                                                                                                                                                                                                                                                                           Obiquitin ligase; SCF; F-box protein; targeted degradation;
                                                                                                                                                                                                                                                                                                                                                                                  F-box protein FWD1p.
                                                                                                                                                                                                                                                                                                                                                                                                          16-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY83254 standard; Protein;
                                                                  Targeting degradation of polypeptide useful for treating cancer and other proliferative disorders, involves conjugating polypeptide with ubiquitin protein ligase or inhibiting ubiquitination using organic
                                                                                                                                                                                                                           08-OCT-1999;
                                                                                                                                                                                                                                                                         WO200022110-A2
                                  Claim 9; Page 184-185; 185pp; English.
                                                                                                                    N-PSDB; AAZ93714.
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                                                                                                                                                       P, Howley P;
                                                                                                                                2000-317970/27.
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The F-box proteins ligases) which can

are a family of ubiquitin be used for the targetted

ligases (SCF ubiquitin degradation of a targe

RESULT 12 AAM78584

AAM78584 standard; Protein; 632

XEXEXEX

06-NOV-2001

(first entry) SEQ ID NO 1246

Human protein

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                             ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                               KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT
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EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN
                                                                KRIVSGAYDGKIKVWDLMAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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98.6%;
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Pred. No. 5
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5.8e-283;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
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Zhao QA,
                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                              Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 3505-3507; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding
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30-NOV-
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                                                                                                                                                                                                                                                                                                                                                                inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; hacmatopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
       181
                                  118
                                                                121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-FEB-2001; 2001WO-US04098
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                                                                                         58
                                                                                                                     61
                                                                                                                                                 15
                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                            _
CLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFV
                                                                        CLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFV 117
                                                                                                               MPSLRCLYNPGTGALTAFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETV 120
                                                                                                                                                                                                    MDPAEAVLQEKALK-----
                                                                                                                                                                                                                                                                                                                    missing at the
                                                                                                                                                                      MDPAEAVLQEKALKFMMEFRSWCPGWNTMARSRLTATSTSRVQCSMPRSLWLGCSSLADS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C,
                                                                                                                                                                                                                                                                                         632 AA;
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 2000US-0496914.
2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0649361.
2000US-0663561.
2000US-0663361.
2000US-0693325.
2000US-0728422.
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, Wang J, Zhang J, Ren F, (
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                  time of publication.
                                                                                                                                                                                                                                              98.6%;
                                                                                                                                 -FMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides with cytokine-like
                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                            Score 2992.5; DB 2
Pred. No. 1.9e-282;
                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                        DB 22; Length 632;
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Wang :
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27-APR-2000; 2000US-0560875.
20-JUN-2000; 2000US-0598075.
19-JUL-2000; 2000US-062325.
01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-0663561.
20-CCT-2000; 2000US-0693325.
30-NOV-2000; 2000US-0728422.
                                                                                          Tang YT,
Zhao QA,
                                                                                       Zhao
                                           WPI; 2001-476283/51.
N-PSDB; AAK52699.
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                                                                                                                                                                                                                                                                                                                                                                                                             Human protein SEQ ID NO 3212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM79566 standard; Protein;
                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                        cytokine;
                                                                             Yang Y,
                                                                                                                                                                                                                                                                                                                                                            ytokine; cell proliferation; cell differentiation; gene therapy;
peptide therapy; stem cell growth factor; haematopoiesis;
rowth factor; immunomodulatory; cancer; leukaemia;
                                                                                         Wang
                                                                                                    Liu C,
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                                                                                                                                                                                                                                                                                                                                                   disorder; arthritis; inflammation.
                                                                           Drmanac RT, Asundi V,
, Wang J, Zhang J, Ren
Wejhrman T, Goodrich R;
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Wang
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Wang ZW;
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Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -

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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
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                                                                                                                                                                                                                                                                                                                                                                                   CLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFV 117
                                                                                                                                                                                                                                                                                                                                       GMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----NSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETV
                                                                                                                  DDTILIWDFLNDPAAQSEPPRSPSRTYTYISR
                                                                                                                                                   DDTILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                                                                                                                                  {\tt FDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSH}
                                                                                                                                                                                                                                                    STCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           568;
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Pred. No. 3.96
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AAM79567 standard; Protein;

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143 CLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFV 58 CLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFV 117

202

MPSLRCLYNPGTGALTAFQNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETV 142

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                                                                                                                                                                                                                                                   The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT, Liu C, Drmanac RT, Zhao QA, Wang D, Wang J, Z Xue AJ, Yang Y, Wejhrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-FEB-2000;
27-APR-2000;
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                                                                                                                                                  Sequence
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                                                                                                                                                                            Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                        treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                      useful in
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19-JUL-2000;
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                                                                                                        Local Similarity
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                                 MDPAEAVLQEKALKFMMEFRSWCPGWNTMARSRLTATSTSRVQCSMPRSLWLGCSSLADS
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   20; Page 286; 6221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                   acids encoding polypeptides with cytokine-like activities, in diagnosis and gene therapy -
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2000US-0620325.
2000US-0654936.
2000US-0663561.
2000US-0663561.
2000US-0693325.
2000US-0728422.
                                                                                           Conservative
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, Zhang J, Ren F, (
n T, Goodrich R;

    Mismatches

                                                                                                        Score 2989.5; DB 2
Pred. No. 3.9e-282;
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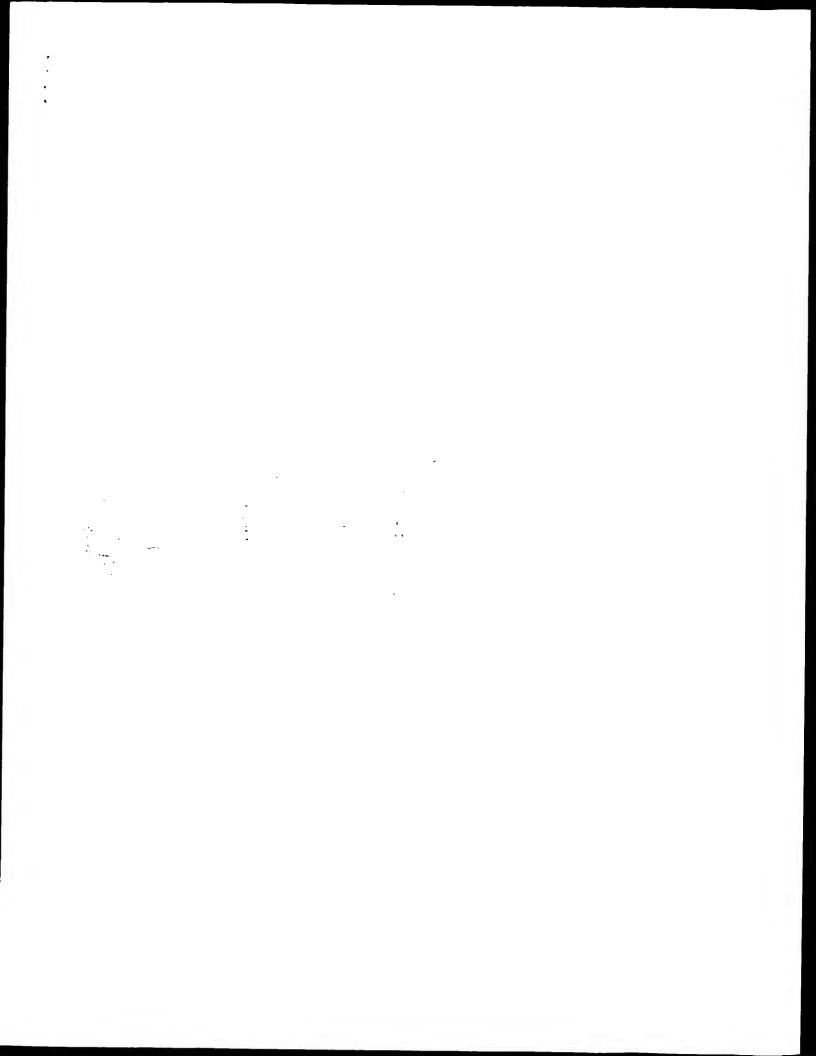
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19-JUL-2000;
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20-OCT-2000;
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27-APR-2000;
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                                                   Xue AJ,
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                                             Wang D,
Yang Y,
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2000US-0634936.
2000US-0663561.
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2000US-0560875.
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, Wang J, Zhang J, Ren F, (
Wejhrman T, Goodrich R;
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              DDTILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                                          FDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSH
                                                                                                                                             STCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIR
                                                                                                                                                                                            GMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNT
                                                                                                                                                                                                                                                                                 ECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNN
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                                                                                                                                                                                                                                                                                                                                                 KIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTL
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                                                             FDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSH
                                                                                                                             STCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIR
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Search completed: February 20, 2003, 09:53:46
Job time : 89 secs



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3034
1 MDPAEAVLQEKALKI
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     DB
TRUB YENDA

TRUB YENDA

FYIB HUMAN

L123_CAEEL

POFB SCHPO

POFL SCHPO

SCOB EMENI

MT30_YEAST

SCO2_NEUCR

SCO2_NEUCR

SCO2_SCHPO

CC4_YEAST

POP2_SCHPO

CC4_YEAST

POP2_SCHPO

CMB_DICDI

YY46_ANASP

YL24_ANASP

YL24_ANASP

LIS1_HUMAN

LIS1_HUMAN

LIS1_HUMAN

LIS1_HOUSE

LIS1_BOUSE

LIS1_BOUS
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091854 xenopus lae
09ukb1 homo sapien
009990 caenorhabdi
  P42527
Q9ukt8
Q9v3j8
Q9v3j8
Q9ugp9
Q60584
Q17963
P47025
P49695
P49695
                                                                                                                                                                                                                                                     Q09855
P87053
Q00659
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caenorhabdi
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drosophila
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kluyveromyc	P56094	TUP1 KLULA	ب	682	و. س	281.5	5
saccharomyc	P16649	TUP1_YEAST	_	713	9.3	283	44
schizosacch	013615	PRP5_SCHPO	Н	473	9.3	283	43
saccharomyc	P38129	T2D4_YEAST	دع	798	9.4	285.5	42
arabidopsis	024456	GBLP_ARATH	ب	327	9.4	286.5	41
homo sapien	014727	APAF_HUMAN	ᆫ	1248	9.5	287	40
brassica na	Q39336	GBLP_BRANA	_	327	9.5	287.5	39
mus musculu	088879	APAF_MOUSE	سا	1249	9.5	289	38
schizosacch	Q09715	TU11_SCHPO	Н	614	9.6	290.5	37
saccharomyc	P36130	YK16_YEAST	_	659	9.6	292	36
rattus norv	Q9epv5	APAF_RAT	Ь	1249	9.7	294.5	35
homo sapien	Q15542	T2D4_HUMAN	<u>.</u>	800	9.8	298.5	34

ALIGNMENTS

CCCCCCCCERRRR	R R R R R R R R R R R R R R R R R R R	RRRRRRRRRRRR RRF 11 1 8 8 X P N X C C C	RESULT FW1A_H FW1A PT 1D F 1D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
"The SCF (beta-TRCP)-ubiquitin ligase complex associates specifically with phosphorylated destruction motifs in I-kappa-B-alpha and beta-catenin and stimulates I-kappa-B-alpha ubiquitination in vitro."; Genes Dev. 13:270-283(1999). -i- FUNCTION: BINDS SPECIFICALLY TO PHOSPHORYLATED IKB ALPHA (PIKAPPABALPHA) AND PHOSPHORYLATED BETA-CATENIN AND PROMOTES THEIR UBIQUITINATION AND DEGRADATION. -I- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEXI- SUBCELLULAR LOCATION: CytoplasmicI- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICINGI- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.	ENCE FROM N.A. (ISOFORM 2). ENCEPBOR 2370; PubMed=9660940; Sttin F., Bour S.P., Durand H., Selig L., Benichou S., Riss D., Strebel K., Benarous R.; ss D., Strebel K., Benarous R.; so I., Strebel K., Benarous R.; cell 1:565-574(1998). NAPP NCE FROM N.A. (ISOFORM 2). NCE FROM N.A. (ISOFORM 2). NCE PROM N.A. (ISOFOR	; Chordate; Primates; Primates (ISOFORM PubMed=98 A., Davin n M., Mernthe recei; 1998).	HUMAN STANDARD; PRT; 605 AA. 69Y297; Q9Y213; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, Created) 16-OCT

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Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50181; FBOX; 1.

PROSITE; PS5018; WD_REPEATS_1; 6.

PROSITE; PS50082; WD_REPEATS_2; 7.

PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conjugation
AIN 190
                  VLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVV 444
VLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVV
                                                                                       SDSTVRVWDVNTGEMLNTL1HHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRR
                                                                                                                                    ETSKGVYCLQYDDQKTVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGS
                                                                                                                                                          ETSKGYYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGS
                                                                                                                                                                                                         GLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRS
                                                                                                                                                                                                                                                                                                                                                                                                                                   NNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTKLANGTSSMIV
                                                                   SDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRR
                                                                                                                                                                                                                                          GLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRS
                                                                                                                                                                                                                                                                           ITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWR
                                                                                                                                                                                                                                                                                                                                                                       PKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDF
                                                                                                                                                                                                                                                                                                                                                                                                                 NNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTKLANGTSSMIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDPAEAVLQEKALKEMCSMPRSLWLGCSSLADSMPSLRCLYNPGTGALTAFQNSSEREDC
                                                                                                                                                                                                                                                                                                          ITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWR 204
                                                                                                                                                                                                                                                                                                                                              PKORKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                603482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00400; WD40; . PF00646; F-box;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF101784; AAD08702.1; -. Y14153; CAA74572.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM00256; FBOX; 1.
SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGNC:1144; BTRC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001680;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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341
381
424
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228 F-BOX.
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94.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 3006;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISSING (IN ISOFORM 2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4C67F3B7E400FD37 CRC64;
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480
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Pfam; PF00400; WD40; 7. Pfam; PF00646; F-box; 1.

InterPro; IPR001810; F-box. InterPro; IPR001680; WD40.

ProDom; PD000018; WD40;

EMBL; M98268; AAA02810.1; -. EMBL; U63921; AAB49671.1; -. EMBL; U63922; AAB49672.1; -.

entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

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Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIANE 3330289; PubMed-8393141;
Spevak W., Keiper B.D., Stratowa C., Castanon M.J.;
"Saccharomyces cerevisiae cdc15 mutants arrested at a late stage anaphase are rescued by Xenopus CDNAs encoding N-ras or a protein with beta-transducin repeats.",
wol. cell. Biol. 13:4953-4966(1993).
                                                                                                                                                                  use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                 the
                                                                                                                                                                                                                 between
                                                                                                                                                                                                                                                                                                                                                                                                                               differential display PCR.";
Dev. Genet. 19:190-198(1996).
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Beta-TrcP (Beta-transducin repeat-containing)
                                                                                                                                                                                                                                                                                                                                                                                       -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 302-518 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FBXW1 OR BTRCP.
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: Probably recognizes and binds to some phosphorylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tdentification of new localized RNAs in the Xenopus oocyte by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ludson J.W., Alarcon V.B., Elinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE - 97109804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRCB_XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              445
                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                    proteins and promotes their ubiquitination SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX)
                                                                                                                                                                                                                                                        SIMILARITY: STRONG, TO C.ELEGANS K10B2.1.
                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS
                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
                                                                                                                                                                                                                                                                                                              NOT INCREASE IN ABUNDANCE IN THE GASTRULA, NEURULA,
                                                                                                                                                                                                                                                                                                                            MATURED OCCYTES: THE LEVEL CHANGE VERY LITTLE EVEN AFTER ZYGOTIC GENE TRANSCRIPTION BEGINS FOLLOWING THE MIDBLASTULA TRANSITION.
                                                                                                                                                                                                                                                                                                                                                         DEVELOPMENTAL STAGE: PRESENT IN FULLY GROWN AND PROGESTERONE-
                                                                                                                                                                                                                                                                                                     TADPOLE EMBRYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=8952061;
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RESULT 3
FW1B_HUMA
ID FW1B,H
AC Q9UKB1
DT 16-OCT
DT 15-UN
DT 15-UN
DE F-BAVAL
GN FBAVAL
GN FBAVAL
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Best Local S
Matches 488
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CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                      Q9UKB1; Q9Y4C6; Q9P2S8; Q9P2S9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
F-box/WD-repeat protein 1B (F-box and WD-repeats
FBXW1B OR FBW1B OR BTRCP2 OR KIAA0696.
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          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                  FW1B_HUMAN
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                                                                                                                                                                                                                                                                                                                        QRIHCRSETSKGYYCLQYDDQKIYSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE
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                                                                                                                                                                                                    YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL
                                                                                                                                                                                                                                 TDITLRRVLYGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ
                                                                                                                                                                                                                                           TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ
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488; Conserv
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WD40;
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91.6%;
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Pred. No. 3
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                                                                                                   PRT;
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A -> AAH (IN REF. 2).
2A52EC19028127F3 CRC64;
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3.9e-188;
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                                                    beta-TrCP2).
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SMAPF; SM00320; "FBOX; 1.

PROSITE; PS50181; FBOX; 1.

PROSITE; PS500678; WD_REPEATS_1; 5.

PROSITE; PS50082; WD_REPEATS_2; 7.

PROSITE; PS50294; WD_REPEATS_REGION; 1.

PROSITE; PS50294; WD_REPEATS_REGION; 1.

PROSITE; PS50294; WD_REPEATS_REGION; 1.

PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                    Ubl conjugation | 129 | 129 | REPEAT | 278 | REPEAT | 318 | REPEAT | 361 | REPEAT | 401 | REPEAT | 442 | REPEAT | 490 | REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20160458;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND ALTERNATIVE
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SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00646; F-box; 1.
PRINTS; PR00320; GPROTEINBRPT
ProDom; PD000018; WD40; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM;
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SMART; SM00320; WD40; 7.
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                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001810; F-b
InterPro; IPR001680; WD4
Pfam; PF00400; WD40; 7.
Pfam; PF00646; F-box; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98403880; PubMed-9734811;
Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
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AB014596; BAA31671.1; ALT_INIT.
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N., Kirikoshi H.,
275
315
398
398
440
478
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527
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CSVPRSLWLGCANLVESMCALSCLQSMPSVRCL
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                                                                                                                                                                                                                   repeat;
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Q09990; QOGNN6;
15-JUL-1998 (Rel. 36, Created)
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
             Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                       Miller N.
                                                            SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                          Kipreos E.T., Gohel S.P., Hedgecock E.M.;
"The Caenorhabditis elegans F-box/WD repeat protein
to limit cell division during development.";
Development 127:5071-5082(2000).
                                                                                                                                                                                                           SEQUENCE FROM N.A., FUNCTION, DEVELOPMENTAL MEDLINE-20515608; PubMed=11060233;
                                                                                                                                                                                                                                                                                                                                                                    F-box/WD-repeat protein lin-23.
LIN-23 OR K10B2.1
                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                     Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 CLKVLTGHTGSVLCLQYDERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFSNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DTILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
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SMART; SM00320; WD40; 7.

PROSITE; PS50081; WD_REPEATS_1; 5.

PROSITE; PS50082; WD_REPEATS_2; 7.

PROSITE; PS500294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                     Matches
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InterPro; IPR001810; P-box
InterPro; IPR001880; WD40.
InterPro; IPR001880; WD40.
Pfam; PF00440; WD40; 7.
Pfam; PF00646; P-box; 1.
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REVISIONS.
                                                     143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U28730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF275253; AAG28037.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted -!- FUNCTI
248 SNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston
                                                                                                                                                                                    148
                                                                                                                                          87
                                                                                                                                                                                                                    27 KPLSIDYLQGHEGLIEEVLKWSEHEQLDFMDKIVHRLSHYQLGKVDNFIRPMLQRDFISN
                                                                                                                                                                                                                                                              88 RKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 7 WD REPEATS (TRE SIMILARITY: STRONG, TO X.LAEVIS FBXW1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (Potential).
DEVELOPMENTAL STACE: Highest levels in embryos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 1 F-BOX DOMAIN. SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
FUNCTION: Functions cell autonomously to negatively regulate cell cycle progression. Required to restrain cell proliferation in
                                                                                                                                                        LPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLA
                                           EKRQWDKFLNISRDMSVRRICEKFNYDVNIKRDKLDQLILMHVFYSKLYPKIIRDIHNID
                                                                                            ERRGWGQYL-----
                                                                                                                                   LPA----HLVELILFNVNSDSLKSCEEVSTSWRCALARGQHWKKLIEKNVRSDSLWWGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         some proteins and promotes their ubiquitination and degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              response to developmental cues. Probably recognizes and binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          levels in larvae. Maternal expression results in high zygotic
                                                                                                                                                                                                                                                                                                                   316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (By similarity)
                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         665 AA;
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA68258.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathway;
127
                                                                                                                                                                                                                                                                                                                                        54.0%;
63.7%;
                                                                                                                                                                                                                                                                                                                                                                                                         75916 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat; WI F-BOX
                                                                                                                                                                                                                                                                                                                   59;
                                                                                     -----FKNKPPDGNAPPNSFYRALYPKIIQDIETIE
                                                                                                                                                                                                                                                                                                                                                             Score 1638.5;
                                                                                                                                                                                                                                                                                                                                                                                                                           ALA-RICH.
G->R: IN LIN-32(RH293)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                                                                                                                                         BF3E9AF51F12ECCC
                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WD repeat.
                                                                                                                                                                                                                                                                                                                                        No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     division;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in embryos and adults,
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DB 1;

Indels Length 665;

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                                                                                RA Wood V. Gwilliam R., Rajandream M.A. Lyne M., Lyne M., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones M., Leather S., Mollean J.,
RA James K., Jones M., Leather S., Mollean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Gliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Gliver K., Simmonds M., Squares R., Squares S., Stevens K.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Weller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Weller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Geffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Locas M., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Daulsen T., Potashkin T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POFB_SCHPO STANDAKD;
Q09855; Q9P7V1;
Q1-FEB-1996 (Rel. 33, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast). Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F-box/WD-repeat protein pof11. POF11 OR SPAC29E6.01 OR SPAC30.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence up 15-JUN-2002 (Rel. 41, Last annotation
Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Systematic genome-wide analysis of F-box protein-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          548
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Best Local Sim
Matches 163;
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Pfam; PF00400; WD40; 7.
Pfam; PF00646; F-box; 1.
PRINTS; PR00320; GPROTEINBRPT
PRODOM; PD000018; WD40; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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-!- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
-!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00256; FBOX; 1. SMART; SM00320; WD40; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z66525; CAA91423.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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InterPro; IPR001680;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
 397
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                                                                                                                                                                                                                                                                                                                                                                              123
                                                                                                                                                                                                                                                                                                                                                   51
                                                                                                                                                                                                                                                                                                                                                                                                                                      67 ENCVAK----TKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLIS 12
                                                                                                                                                                                                                                                                                                                                                                                                           æ
YNGKFIYSGSSDLTIRIFEASSGKLLRMLQGHEDLIRTVRFNDEKIYSGGYDGTVRIWN-
                         YRDRLYVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL 497
                                                                                                                                                                                                                                                                                          LEDPGIWKALYMQKGWFVNENVLNEFEAWRRTHKFPQPRFENFLKQQNIIGPYGTMFLPQ 166
                                                                                                                                                                                                                                                                                                                                                                                                           KNVVSKVSDLTSCSDFSTSSPVPCLNPLS--
                                                                                   ITLRRVLVGHRAAVNVVDFDDK--YIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ
                                                                                                               SGSSDSTIIIWDWQNRRPLKVYFGHTDNVLGVVVSENYIISSSRDHTARVWRLDATSPAE
                                                                                                                                           TGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVW--DMASPTD 379
                                                                                                                                                                       RATLDSVYCVQYDDEIMVSGSKDRTVSVWDVNSRFILYKLYGHSGSVLCLDFCRRRNLLV
                                                                                                                                                                                                  -ETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDER--VII 321
                                                                                                                                                                                                                               QFIF-----DSNGRPLLNWSYLY----KEHAHLDSNWRHGRFLVSTFNNPSIRFPADQDF 217
                                                                                                                                                                                                                                                            QYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRS------
                                                                                                                                                                                                                                                                                                                       TSDGMLWKKLI - - - -
                                                                                                                                                                                                                                                                                                                                                   SLSKEGVVAVYNHVRSLLFTDFTEVFP----EEVSLRVFSYLDQLDLCKCKLMSKRWKRL 106
                                                                                                                                                                                                                                                                                                                                                                              QMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRV 182
                                                      ACM-HYLRGHLASVNSVQYSSKTGLIVTASSDRTLRTWDITTGHCIRIIHAHQRGIACAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB061694; BAB55543.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS50294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS50181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS50082;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WD_REPEATS_1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FBOX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116
256
298
338
386
464
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                                                                                                                                                                                                                                                                                                                      -ERMVRTDSLWRG------LAERRGWG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F-BOX
WD 1.
WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
WD 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CEF34D4EFFBC2E10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 506;
                                                                                                                                                                                                                                                                                                                                                                                                           -HENNRIDLIRDLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Вþ Š

498 VAALDPRAPAGTLCLRTLVEH------SGRVFRLQFDEFQIVSSSHDDTILIWDF 546

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RX MEDLINE=2184401; PubMed=11859360;
RX MEDLINE=2184401; PubMed=11859360;
RA MOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hint S., Jagels K.,
RA Holroyd S., Mounes L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Jammonds M., Squares R., Squares S., Stevens K.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R., C., Tivey A., Walsh S.V., Warrer T., Whitehead S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moseft D., Hilbert H.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V. Ussery D., Barrell B.G., Nurse P.;
RE Nature 415:871-880(2002).
CC 1- FUNCTION: Probably recognizes and binds to some phosphorylated
CC 1- SUBUNIT: PART OF A SCF (SKP1-CULIN-F-BOX) PROTEIN LIGASE COMPLEX
CC 1- SUBUNIT: PART OF A SCF (SKP1-CULIN-F-BOX) PROTEIN LIGASE COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P87053;
P5-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
F-box/WD-repeat protein pof1 (Skp1-binding protein 1).
POF1 OR SBP1 OR SPAC57A10,05C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Katayama S., Kitamura K., Toda T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Systematic genome-wide analysis of F-box protein-encoding genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            456 -----FNTGEQHCVLHNSRNSRVFGLQFDHRRIIACTHSSEILVWNF 497
                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                          (BY SIMILARITY)
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DI DI

16-OCT-2001 (Rel. Sulfur metabolite 15-JUL-1998 15-JUL-1998

(Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 40, Last annotation updat

repression control protein

SCOB_EMENI RESULT 7

200659; SCOB_

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STANDARD;

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678 B

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AB032410; BAA84528.1;
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Best Local
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REPEAT
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InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 7.
Pfam; PF00646; F-box; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z94864; CAB08168.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00320; GPROTEINBRPT. ProDom; PD000018; WD40; 5.
         497
                                                      493 KVWDLVAALDPRAPAGTICLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDP 550
                                                                                                                               437
                                                                                                                                                                                                                                                   381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 KPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERM 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ONSILE, WORLD TO THE PROPERTY OF THE PERT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 ---CRQVVLSGHSDGVMCLQLVRNILASGSYDATIRLWNLATFQQVALLEGHSSGVTCLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 RIHCR----SETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQ 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 DYPTSSNEETISSVKPPSPNSDSKFFLPFKTRPWKEVYAERCR----VECNWRHGR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 VRTDSLWRGLAERRGWGQYLFKN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 DSLVRLDFLSLLPV----EISFRILSFLDARSLCQAAQVSKHWKELADDDVIWHRMCEQH 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 SSMIVPKQRKLSASYEKEKELCVKYFEQWSE---SDQVEFVEHLISQMCHYQHGHINSYL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 SSM----HNELSGLSEKSRQRVEAVWAAFSEASCSERKLALQGILNNCSSSLLSFASSTL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
KVWEACE-----CVHTLKNHSEPVTSVALGDCEVVSGSEDGKIYLWLFNNAP
                                                                                                                      VQSLALADSRLFSCSLDGTIKQWDIEKKKCVHTLFGHIEGVWEIAADHLRLISGAHDGVV 496
                                                                                                                                                                                                                                                                                                   ASPTDITLRRVLVGHRAAVNVVDF---DDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRG 432
                                                                                                                                                                                                                                                                                                                                                               FDQCKLISGSMDKTIRIWNYRTSECISILHGHTDSVLCLTFDSTLLVSGSADCTVKLWHF 380
                                                                                                                                                                                                                                                                                                                                                                                                                         YDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDM 374
                                                                                                                                                                               IACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKI 492
                                                                                                                                                                                                                                         SGGKRITLR----GHTGPVNSVRIIRDRGLVLSGSDDSTIKIWSLETNTCLHTFSAHIGP 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INRK-----CEKCGWGLPLLERNTLYAAKASIQKRYERLTKRGVDQAHESSPVKKAKLD 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         605 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KPPDGNAPPNSF-----YRALYPKIIQDIETIESNWRCGRHSLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WD_REPEATS_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WD_REPEATS_1;
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500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.5%; Score 590.5; 29.0%; Pred. No. 5.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86; Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F-BOX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 5.5e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7118C9379EC5C1F0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50181; FBOX; 1.

PROSITE; PS00678; WD_REPEATS_1; 4.

PROSITE; PS50082; WD_REPEATS_2; 7.

PROSITE; PS50294; WD_REPEATS_REGION;

Transcription_regulation; Repeat; WD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=5072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCONB OR MAPB1
                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00400; WD40; 7 Pfam; PF00646; F-box;
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InterPro; IPR001680;
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                                                                                                                                                                                                                                                                                                                                               REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U21220; AAC15905.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                117 VEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVC 176
                                                                                                                                                                                                                                                                                        Loca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPRESSION.

SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).

SIMILARITY: CONTAINS 1 F-BOX DOMAIN.

SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY OF WD-REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEINS
                                                                                                                                                                                                                      LQGIMAQCCFPQLSYISATVRDLIRIDFITALP----PEIAFKILCYLDTTSLCKASQVS 208
TETGEELRTLRGHESGIRCLQFDDTKLISGSMDRTIKVWNWRTGECISTYTGHRGGVIGL 435
                          KNTLECKRILTGHTGSVLCLQYDERVIITGSSDSTYRVWDVNTGEMLNTLIHHCEAVLHL 353
                                                                                 KIIQDIETIESNWRCGRHSLQRIHCRSETSK----GVYCLQYDDQKIVSGLRDNTIKIWD 293
                                                                                                            DKGVVGPRSPDASAESPPSGKRKLEDDEVAVVKRHCSSLGSDAGVDKDSDFFKTRYRPWK
                                                                                                                                        ------PPDGNA--PP-----
                                                                                                                                                                  RGWRALADDDVVWHRMCEQHIHRK-----CKKCGWGLPLLDRKRLRESKREIELRATTW 262
                                                                                                                                                                                             KEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNK------
                                                     EVYKDRFKVGTNWKYGR------CSIKTFKGHTNGVMCLQFEDNILATGSYDTTIKIWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00256; FBOX;
SM00320; WD40;
                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                 76070 MW;
                                                                                                                                                                                                                                                                                        19.0%; Score 575; DB 1; 26.9%; Pred. No. 9.4e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN THAT
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                                                                                                                                         ----- NSFYRALY---P 237
                                                                                                                                                                                                                                                                                                       Length 678;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     he EMBL outstation restrictions on it
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                         modified and this statement is not removed. Usage by and for common or send an email to license@ieh----
                                                                                                                                                                                                                                                                                                                                                                                                                                                adenosylmethionine, is an essential protein with WI40 repeats."; mol. Cell. Biol. 15:6526-6534(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MT30_YEAST
           EMBL; Z46861; CAA86905.1;
EMBL; L26505; AAA96717.1;
SGD; S0001308; MET30.
                                                                                                                                                                                                         -i- SUBUNIT: SEEMS TO INTERACT WITH MET4.
-i- SIMILARITY: CONTAINS 1 F-80X DOMAIN.
-i- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
-i- SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=S288c / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Surdin-Kerjan Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thomas D., Kuras L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=X2180-1A;
MEDLINE=96069360; PubMed=8524217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MET30 OR YIL046W.
                                                                                                                                                This SWISS-PROT entry is copyright. It is produ between the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Met30p, a yeast transcriptional inhibitor that responds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               436
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                                                                                                                                                                                                                                                                      GENES EXPRESSION
                                                                                                                                                                                              PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barbey R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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DOMAIN 181 227
REPEAT 300 328
REPEAT 340 368
REPEAT 380 408
REPEAT 419 449
REPEAT 461 499
REPEAT 500 578
REPEAT 550 578
REPEAT 607 635
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PROSITE; PS00678; WD_REPEATS_1; 4.
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION;
                                                                         583
                                                                                                                                                            449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00320; GPROTEINBRPT. ProDom; PD000018; WD40; 4.
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Pfam; PF00400; wD40; 7
Pfam; PF00646; F-box;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 ASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPAR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 LPEYNFTKFCYRHNPDIQFSPTHTACYKQDLKRTQEINANIAKLPLQEQSDIHHIISKYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 IPEKNSLRQTYNSCARLCLN-QETVCLASTAMKTENCVAK-TKLANGTSSMIVPKQRKLS 91
                                                                   -----KCMHTF---NGR--RLQRETQHTQTQSLGDKV 609
                                                                                              RAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTI 541
                                                                                                                        LSCGLDNTIKLWDVKTGKCIRTQFGHVEGVWDIAADNFRIISGSHDGSIKVWDLQSG---
                                                                                                                                                                               VQKIIPLTIKDVENLATDNTSDGSSPQDDPTMTDGADESDTPSNEQETVLDENIPYPTHL
                                                                                                                                                   -----DNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDP
                                                                                                                                                                                                                  KRGIACLQYRD--RLVVSGSS---------
                                                                                                                                                                                                                                       ESRTCYTLR----GHTEWVNCVKLHPKSFSCFSCSDDTTIRMWDIRTNSCLKVFRGHVGQ 465
                                                                                                                                                                                                                                                                  ASPTDITLRRVLVGHRAAVNVVDFDDKYI--VSASGDRTIKVWNTSTCEFVRTLNGH---
                                                                                                                                                                                                                                                                                              FDDRKLITGSLDKTIRVWNYITGECISTYRGHSDSVLSVDSYQKVIVSGSADKTVKVWHV
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                                                                                                                                                                                                                                                                                                                                                    --HCRIQEFKGHMDGVLTLQFNYRLLFTGSYDSTIGIWDLFTGKLIRRLSGHSDGVKTLY 349
                                                                                                                                                                                                                                                                                                                                                                               RIHCRSETSK----GVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQ 314
                                                                                                                                                                                                                                                                                                                                                                                                            PNCGWGLPLLHMKRARIQQNSTGSSSNADIQTQTTRPWKVIYRERFKVESNWRKG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                       ---GWGQYLFKNK------PPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --QELSLKILSYLDCQSLCNATRVCRKWQKLADDDRVWYHMCEQHI------DRKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERR- 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SM00256; FBOX; 1.
SM00320; WD40; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    640 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WD 2.
WD 3.
449 WD 4.
499 WD 5.
ND 6.
WD 8 (POTENTIAL).
M -> I (IN REF. I).
5135D4BCAZELEB97 C.
9 545; DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
72835 MW;
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PRT;
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650 AA
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Best Local S
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REPEAT
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REPEAT
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               209
                                                                                      223
                                                                                                                                                                 155
                                                                                                                                                                                                                                                                                                                                                                     117 VEHLISOMCHYOHGHINSYLKPMLORDFITALPARGLDHIAENILSYLDAKSLCAAELVC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00320; GPROTEINBRPT ProDom; PD000018; WD40; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00400; WD40; 7 Pfam; PF00646; F-box;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U17251; AAA68968.1; -. TnterPro: IPR001810; F-box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The sulfur controller-2 negative regulatory gene of Neurospora crassa encodes a protein with beta-transducin repeats.";
Proc. Natl. Acad. Sci. U.S.A. 92:3343-3347(1995).
-!- FUNCTION: NEGATIVELY REGULATES SULFUR STRUCTURAL GENE EXPRESSION.
-!- INDUCTION: EXPRESSED ONLY UNDER LOW-SULFUR CONDITIONS.
-!- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
-!- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
                                                                                                                                                                                                                                           177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
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InterPro; IPR001680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurospora crassa.

Neurospora crassa.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariales; Sordariaceae; Neurospora.
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -
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15-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95241499; PubMed=7724564;
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                                                                                                                                                                                                                                                                                           99 LQGILSQLCFPQLSFVSREVNEALKIDFISALPV----ELAQKVLCYLDTVSLTKAAQVS 154
QGRVTELADSHDSQDRSVNQHGKRPAAEAEEEDPIKKRQCMAAAEASKAVTQPKTRSWKA
                                                                                      DGNA---
                                                                                                                                         QRWRTLADSDAVWVRMCEQHVNRK-----CTKCGWGLPLLERKKLRNYTRQRQLAKGGP
                                                                                                                                                                                                                        KEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     650 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170
320
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400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.5%; Score 531.5; DB 1; 25.0%; Pred. No. 1.7e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72189 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SCON2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WD40
                                                                                                                                                                                                                                                                                                                                                                                                                                                76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WD 1. WD 2. WD 3. WD 4. WD 5. WD 7. WD 7. WD 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7473859C99F1B028 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        180;
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RESULT 10
SE10_CAEEL
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Pfam; PF00400; WD40; 7.
Pfam; PF00646; F-box; 1.
PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 5.
SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEIO_CAEEL STANDARD; PRT; 579 AA (937)94; (15-JUL-1998 (Rel. 36, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Sel-10 protein.
                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones S.J.M.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
-!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sims M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sel-10 protein.
SEL-10 OR F55B12.3.
                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                              InterPro; IPR001680;
                                                                                                                                                                                                      InterPro; IPR001810; F-box.
                                                                                                                                                                                                                                     WormPep; F55B12.3; CE16120.
                                                                                                                                                                                                                                                                EMBL; Z79757; CAB02129.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVISIONS
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                                                                                                                 NTIRLWDI ---
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                                                                                                                                                                                                                                                                               CDLNVHRFLKLQKFGDIFERAADKSRYLRADKIEKNWNANPIMGSAV-LRGHEDHVITCM
                                                                                                                                                                                                                                                                                                      PN-SFYRALYPKIIQDI-----
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                                                                                                                                                                                                                                                                                                                                                                                                FVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELV 175
                                               EGT-CVHMLSGHRSAITSLQWFGRNMVATSSDDGTVKLWD
                                                                    AGTICLRTIVEHSGRVFRLQ-FDEFQIVSSSHDDTILIWD 545
                                                                                           TSIRVWDFTRPEGQECVALLQGHTSLTSGMQLRGNILVSCNADSHVRVWDI---
                                                                                                                                         AVRCVQFDGTTVVSGGYDFTVKIWNAHTGRCIRTLTGHNNRVYSLLFESERSIVCSGSLD 431
                                                                                                                                                              AVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDR--LVVSGSSD 449
                                                                                                                                                                                      WSTVDGSLLHTLQGHTSTVRCMAMAGSILVTGSRDTTLRVWDVESGRHLA - - - TLHGHHA
                                                                                                                                                                                                          WDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRA
                                                                                                                                                                                                                                   QIHDDVLYTGSDDNTLKVWCIDKGEVMYTLVGHTGGVWTSQISQCGRYIVSGSTDRTVKV
                                                                                                                                                                                                                                                                                                                            SKNWKLISEIDKIWKSLGVEEFKHHPDPTDRVTGAWQGTAIAAG-
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PS00678;
PS50082;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FBOX; 1. WD_REPEATS_1;
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28.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 520; Db 1; Pred. No. 1.1e-31; Mismatches 222;
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WD 1.
WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
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RC p53699;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2091 (Rel. 40, Last annotation update)
DT 02-C201 (Rel. 40, Last annotation update)
DE Cell division control protein 4.

GN CDC4.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina;
OC Saccharomycetales; mitosporic Saccharomycetales;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-SGY126;
RN Shieh J.C., White A.M., Rosamond J.;
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Saccharomycetes;

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SOFT TO THE TOTAL DESCRIPTION OF THE TOTAL DES
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PROSITE; PS500878; WD_REPEATS_1; 4.

PROSITE; PS50082; WD_REPEATS_2; 4.

PROSITE; PS50294; WD_REPEATS_REGION; 1.

Cell_division; Mitosis; Sporulation; Repeat; WD_repeat.
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-I- FUNCTION: THIS PROTEIN IS ESSENTIAL FOR INITIATION OF DNA
REPLICATION AND SEPARATION OF THE SPINULE POLE BODIES TO FORM
POLES OF THE MITOTIC SPINULE. IT ALSO PLAYS A ROLE IN BUD
DEVELOPMENT, FUSION OF ZYGOTIC NUCLEI AFTER CONJUGATION AND
VARIOUS ASPECTS OF SPORULATION. REQUIRED FOR HTA1-HTB1 LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 SEANQNHLVFKLLQKTTRPTLSTFNNLINNSLKRDILSNVPF----EVTMKILSYLDYKT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 SESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001810;
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SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
GHLDRVYSTAIDFHSKTCFSGSMDSNINVWNFETGELKKVLVGHASLVGLLDLVDDVLVS
                                                         GH--RAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVS 445
                                                                                                                  YIETFEGEFDNPYLIAVLSGHTQSVRSISGYGNIIISGSYDSTVRVWDLLDDGHCTHVLQ 518
                                                                                                                                                                                                                                                                                                 NTLTHH-----CEAVLHL----RENNG------MMVTCSKDRSIAVWDM-----
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                                                                                                                                                                                                                                           HIFRGHTSTIRCLDIIHPAVIGKNQDGEDIVFPEYPLLITGSRDHNIHVWKLPVVDDSQD 458
                                                                                                                                                                                                                                                                                                                                                                 VTGVDDKCISIYSTQTGQLMKVLEGHEGGVWALKYTGNTLVTGSTDRTVRVWNMKTGQCT 398
                                                                                                                                                                                                                                                                                                                                                                                                                           VSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEML 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REWSTLPEINSAQVLYKK----RKIIVNRWMDPKFKPHRISVSGHGNKVVTCLQHDDEKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLSVAQVCKKWFDIINNPDTWIKLLKRDKLITDDAVIK-----YELQYPDQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00256; FBOX; 1.
SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        684 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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351
391
431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.7%; Score 477.5;
25.4%; Pred. No. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76090 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rmatics Institute. There are no rest institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F-box.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WD 1.
WD 2.
WD 3.
WD 4 (POTENTIAL).
WD 5.
WD 6.
WD 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F-BOX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                     -ASPIDITLR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .1e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 121;
                                                                                                                                                                                  --RVLV 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                        374
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QΥ 밁

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δÃ 밁 δõ Db Ş В Qy Db Qy

Matches 164;

Similarity

Conservative

102;

Mismatches

Indels 145;

Gaps

30;

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  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                           REPEAT
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REPEAT
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REPEAT
                                                                                                                                                                                                                             GTP-binding;
                                                                                                                                                                                                                                      SMART; SM00320; WD40; 10.

PROSITE; PS50837; NACHT 1.

PROSITE; PS00078; WD_REPEATS_1; 10.

PROSITE; PS50082; WD_REPEATS_2; 10.

PROSITE; PS50294; WD_REPEATS_REGION;

GTD_big41c, PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                            PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 10.
                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001680; WD40. Pfam; PF00400; WD40; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                beta homologous domain.";
Gene 162:135-139(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saupe S., Turcq B., Begueret J.;
"A gene responsible for vegetative incompatibility in the fungus Podospora anserina encodes a protein with a GTP-binding motif and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update
Vegetatible incompatibility protein HET-E-1.
                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                        EMBL; L28125; AAA85775.1;
                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q00808;
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=96009891; PubMed=7557402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Pe
Sordariales; Lasiosphaeriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=5145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HET L_PODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Podospora anserina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          630 EKGTFARDLLSDVTGGIWQVRFDYKRCVAAVQRIINEDEGETFIEILDF-SQPLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          446 GSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 10 WD REPEATS (TRP-ASP DOMAINS). SIMILARITY: CONTAINS 1 NACHT DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: RESPONSIBLE FOR VEGETATIVE INCOMPATIBILITY THROUGH SPECIFIC INTERACTIONS WITH DIFFERENT ALLELES OF THE UNLINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HET -C
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                                                                                                                1007
                                                                                                                                                                                                                              Repeat;
                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                629
307
869
911
953
995
1037
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  15.0%;
26.0%;
                                                                                                                                                                                                                           WD repeat
                                            149765
                                                      NACHT.
GTP (I
WD 1.
WD 2.
WD 3.
WD 4
WD 5
WD 6
WD 6
WD 7
WD 7
WD 7
                                            M.
Score 455.5; DB 1; Pred. No. 2.3e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Podospora
                                          965FB319844E0651 CRC64;
                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1356 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
             Length 1356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNLINKED
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                                                                                                                                                                                                                                                                                                                                                                     POP1_SCHPO STANDARD; PRT; 775 AA. P87060; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycete
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1090
                                                                                   "Fission yeast WD-repeat protein pop1 regulates genome ploidy through ubiquitin-proteasome-mediated degradation of the CDK inhibitor Rum1 and the 5-phase initiator CdC18.";
                                                                                                                                                                                                                                                                                                                                         WD-repeat protein pop1. POP1 OR SPBC2G2.18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1141 VAFSPDGQRVASGSIDGTIKIWDAASGTCTQ 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1030
                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           581
                                                                                                                                                                   MEDLINE-97347242;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                409
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MEDLINE=21848401; PubMed=11859360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     701 WIDHLRDLVSSTSSKWVHLLQDDGDIHRFLTTKYLYWLEALSLLRALP-EGINAIRQLES
                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQF--DEFQIVSSSHDDTILIWDFLNDPAAQ 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKNKPPDGNAPPNSFYRALY----PKIIQDIETIESNWRCGRHSL--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QHGHINSYLKP-----MLQRD----FIT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMPDDVSDDPESLEEIVKLCGSFLIIRERTVYFVHQSAKDFLLGTASDKASNKASQEAFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGHEELVRCIRF -- DNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFR 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \tt DKTIKIWDTASGTCTQTLEGHGGWVQSVVFSPDGQRVASGSDDHTIKIWDAVSGTCTQTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRTIKVWNTSTCEFVRTLNGHKRGIACLQYR--DRLVVSGSSDNTIRLWDIECGACLRVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAFSPDGQRVASGSGDKTIKIWDTASG---TCTQTLEGHGGSVWSVAFSPDGQRVASGSD 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRFN-NGMMVTC-SKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDF---DDKYIVSASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASGTCTQTLEGHGGRVQSVAFSPDGQRVASGSDDHTIKIWDAASGTCTQTLEGHGSSVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTLECKRILTGHTGSVLCLQY--DERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQRVASGSDDKTIKIWDTASGTGTQTLEGHGGSVWSVAFSPDRERVASGSDDKTIKIWDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLGHTIRGRLIA---IVRDGYRF---ALSYRMIIEKAPLQAYTSAL------V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIER----MVRTDSLWRGLAERRGWGQYL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGHGDSVWSVAFSPDGQRVASGSIDGTIKIWD-----AASGT-CTQTLEGHGGWVHS
                                                                       11:1548-1560(1997)
                                                                                                                                                                   PubMed=9203581;
                                                                                                                                                                                                                                                                                                   Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -ALPARGLDHI -- AEN 159
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   Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Ste
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.
                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99144318; runneu ..... Toda T.;
Kominami K.-I., Ochotorena I., Toda T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complexes together with cullin-1 in fission
F-box) ubiquitin ligase.";
                                   REPEAT
REPEAT
                                                                         Repeat;
                                                                                                   PROSITE; PS50181; FBOX; 1.

PROSITE; PS00678; WD_REPEATS_1; 3.

PROSITE; PS50082; WD_REPEATS_2; 4.

PROSITE; PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                       EMBL; AL022103; CAA17898.1; InterPro; IPR001810; F-box.
                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes Cells 3:721-735(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-972;
                                                                                                                                                                                     PRINTS; PR00320; GPROTEINBRPT.
PRODOM: PD000018; WD40; 3.
SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION:
                                                                                                                                                                                                                                                                     Piam;
                                                                                                                                                                                                                                                                                                     InterPro; IPR001680;
                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: Homodimer and heterodimer with pop2. Binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                are subsequently ubiquitinated and targeted to the for degradation. % \label{eq:control_eq}%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Involved in maintenance of ploidy through proteasome dependent degradation of CDK inhibitor ruml and S-phase initiator cdc18. Functions as a recognition factor for ruml and cdc18, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cdc18
                                                                                                                                                                                                                                                                   PF00400; WD40; 7
                                                                                                                                                                                                                                                                                                                                                               Y08391; CAA69671.1; -.
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repeat.
298
444
484
575
615
 345
472
538
603
                                                                                                                                                                                                                                                                                                         WD40
   F-BOX
WD 1.
WD 2.
WD 3.
WD 4.
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RESULT 14
CC4_YEAST
ID CC4_YEAST
ID 01-AU
AC P0788
AC P0781
AC P0781
AC P0781
AC P0781
O1-AU
DT 01-AU
DT 15-JU
DE Cell
GN CDC4
OS Sacch
OC EUKAI
OC Sacch
OC Sacch
OC Sacch
COL
TILL
RN [1]
RN [1]
RN SEQUE
RX MEDLI
RA YOChe
RT A TLIU
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                                                                                                                                                                       CC4_YEAST STANDARD; PRT; P07834; 01-AUG-1988 (Rel. 08, Created) 01-NOV-1995 (Rel. 32, Last sequenc 15-UUN-2002 (Rel. 41, Last annotat Cell division control protein 4. CDC4 OR YFL009W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
              J. Mol.
[2]
                                         a related pseudogene.
                                                                               MEDLINE=88011240; PubMed=3309335;
                                                                                                                       NCBI_TaxID-4932;
                                                                                                                                  Eukaryota; Fungi; P
Saccharomycetales;
                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
SEQUENCE
                                                "Structural comparison of the yeast
                                                                 Ochem J., Byers B.
                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             661
                                                                                                                                                                                                                                                                                                                                                                                  610
                                                                                                                                                                                                                                                                                                                                                                                                           463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 LCLQYDERVIITGSSDSTYRVWDYNTGEMLNTLIHHCEAVLHLRFNNGMMYTCSKDRSIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 TFSLDAPNNSVNYSYFSPNLLGNDSKTRQSFPPHSSSSSHNSLHEPVIYDFSSENPSIHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 REKCLKRRNSSLSSNLHANKRFLFNSQSDGNKKNETFPSTNYSNVFYPNNCDSKEVASET 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 RHSLQRIHCRSETSKGVYC---LQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 SNHLSSQKNAVLKLAQLISSFEKLPESVRQYLLFHLLSRCGKHAVQNIHKILLPIFQKNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 VC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 QEKALKFMNSSEREDC------NNGEPPRKIIPEKNSLRQTY-NSCARLCLNQET 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                            LVSQVTFNQNILVSASAPPDTSLRVWD 687
                                                                                                                                                                                                                                                                                                                                                  RVFRLQFDEFQIVSSS--HDDTILIWD 545
                                                                                                                                                                                                                                                                                                                                                                                                     LRVLEGHEELVRCIRFDNKR--IVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSG
                                                                                                                                                                                                                                                                                                                                                                                                                              NPDQNNDFTSATTNPFYIRTLRGHTDSVREVACL---GDLIVSASYDGTLRVWKASTGVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TSTCEFVRTLNGHK----RGIACLQYRDRLVVSGSSDNTIRLWDIECGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DVEKE-----NRPASNDANSMPPYIISSSRDCTIRLWSLPCLDDPPFVNVNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWN--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTGFPA----EITNLVLTHLDAPSLCAVSQVSHHWYKLVSSNEELWKSLFLKDGFFWDSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LHAPEKIKRCSFPIHGVRLITKLQFDDDKIIVSTCSPRINIYDTKTGVLIRSLEEHEGDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSKIRTMCLEQSLSA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYR-VTSDGMLWKKL-----I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----SYEKEKEL-----CVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDF 144
                         Biol. 195:233-245(1987).
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775 AA;
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                                                                                                                                  Ascomycota; Saccharomycotina; Saccharomycetaceae; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             687
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25.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 453; DB 1;
Pred. No. 1.7e-26;
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                                                cell division cycle gene CDC4 and
                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                         779
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                                                                                                                                 Saccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229; Indels 150;
                                                                                                                                               Saccharomycetes;
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Best Local
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                                                                                                                                                                                                                                     REPEAT
REPEAT
                                                                                                                                                                                                                                                                                          DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                             REPEAT
169 LCAAELVCKEWYR-VTSDGMLWKKLI--ERMVRTDSLWRGLAERRGWGQYLFKNKPPDGN 225
                                                                                                                                                                                                                                                                  REPEAT
                                  245
                                                           109
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PROSITE; PS00678; WD_REPEATS_1; 4. PROSITE; PS50082; WD_REPEATS_2; 5. PROSITE; PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00256; FBOX; SMART; SM00320; WD40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00320; GPROTEINBRPT ProDom; PD000018; WD40; 4. SMART; SM00256; FBOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGD; S0001885; CDC4.
InterPro; IPR001810;
InterPro; IPR001680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D50617; BAA09229.1;
EMBL; Z46255; CAA86341.1;
PIR; A26867; A26867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-S288c / AB972;
Barrell B.G., Churcher C., Rajandream M.A.;
Submitted (SEP-1994) to the EMEL/GenBank/DDBJ databases.
-i- FUNCTION: THIS PROTEIN IS ESSENTIAL FOR INITIATION OF DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00400; WD40; Pfam; PF00646; F-box;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X05625; CAA29113.1; -.
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Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama
Yamazaki M., Tashiro H., Eki T.;
"Analysis of the nucleotide sequence of chromosome VI from
Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=S288c / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-579 FROM N.A.
                                                                                               194 TTPLAKTTKTINN------NNNIADLIESKDSIISPEYLSDEIFSAINNNLPHAYFK--
                                                                                                                                         56 TYCLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEK------ELCVKYFEQW 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSCRIPTION ACTIVATION.
SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPLICATION AND SEPARATION OF THE SPINDLE POLE BODIES TO FOR POLES OF THE MITOTIC SPINDLE. IT ALSO PLAYS A ROLE IN BUD DEVELOPMENT, FUSION OF ZYGOTIC NUCLEI AFTER CONJUGATION AND VARIOUS ASPECTS OF SPORULATION. REQUIRED FOR HTAL-HTB1 LOCUS
                                             SESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKS 168
-----NLLFRLVANMDRSELSDLGTLIKDNLKRDLITSLPF----EISLKIFNYLQFED
                                                                                                                                                                                                   139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genet. 10:261-268(1995).
                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS50181; FBOX;
                                                                                                                                                                                                                                                                                           460
779 AA;
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitosis;
2 319
                                                                                                                                                                                                                                                                                                                                                                                                                                       408
449
493
                                                                                                                                                                                                                                                                                                                                                                                          598
                                                                                                                                                                                                                       13.2%;
                                                                                                                                                                                                                                                                                             86089 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F-box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WD40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sporulation; F-BOX.
                                                                                                                                                                                              80;
                                                                                                                                                                                                           Score 399; Db ...
                                                                                                                                                                                                                                                                                                                                        WD 2. WD 3. WD 5. WD 5. WD 7.
                                                                                                                                                                                                                                                                                                                    K -> E (IN REF.
                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                           0348F2F8FA78F3BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat;
                                                                                                                                                                                                                                      DB 1; Length 779;
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MEDLINE=21848401; PubMed=11859360;
MCOd V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Hukkle E.J., Hunt S., Jagels K.,
Holroyd S., Hornsby T., Jones M., Leather S., McDonald S., McLean J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
WD-repeat protein pop2 (Proteolysis factor su
pop2 OR SUD1 OR SPAC4D7.03.
Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                MEDLINE=99318628; PubMed=9653157;
Jallepalli P.V., Tien D., Kelly T.J.;
"sudl+ targets cyclin-dependent kinase-phosphorylated Cdcl8 and Ruml proteins for degradation and stops unwanted diploidization in fission
                                                                                                                                                                                                                                                                                                                                MEDLINE-99227353; PubMed-10209119; Wolf D.A., McKeon F., Jackson P.K.; "F-box/WD-repeat proteins poplp and Sudlp/Pop2p form complexes that bind and direct the proteolysis of cdc18p."; Curr. Biol. 9:373-376(1999).
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Query Match
Best Local :
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                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kominami K.-I., Ocholorena I., Toda T.;

"Two F-box/WD-repeat proteins Popl and Pop2 form hetero-and homo-
"Two F-box/WD-repeat proteins Popl and Pop2 form hetero-and homo-
complexes together with cullin-1 in fission yeast SCF (Skip-cullin-1-
F-box) ubiquitin ligase.";

Genes Cells 3:721-735(1998).

-!- FUNCTION: Involved in maintenance of ploidy through proteasome
dependent degradation of CDK inhibitor ruml and S-phase initiator
cdcl8. Functions as a recognition factor for ruml and cdcl8, which
are subsequently ubiquitinated and targeted to the 26S proteasome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Squares Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Gabel C., Fuchs M., Fritzc C., Lehrach H., Reinhardt R., Pohl T.M., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
                                                                                                         REPEAT
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                                                                                                                                                                           Repeat;
                                                                                                                                                                                                                                                                                                                                                      Interpro: IPR001810; F-box.
Interpro: IPR001680; WD40.
Pfam; PF00400; WD40; 7.
Pfam; PF00646; F-box; 1.
                                                     SEQUENCE
                                                                                                                                                                                                                                                                                SMART; SM00256; FBOX; 1. SMART; SM00320; WD40; 6.
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                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                   PRINTS; PR00320; GPROTEINBRPT ProDom; PD000018; WD40; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
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SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
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PS50082;
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3: /cgn2_6/ptodata/1,
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-914-999-7
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US-08-923-463-11
US-08-283-917-8
US-08-282-463-14
US-08-188-582-17
US-08-646-715-17
US-08-646-596B-1
US-08-738-367-6
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JR-2 KINASE (CTGCCAGCTCGGGGATTGGATCATATCGCTGAAACATTCTGTCATACCTGGATGCCAAA [24.4; DB 4; D. 6.2e-31; atches 1;	GENES	-032-742-3 -032-742-21 -032-742-24 -032-742-25 -961-527-103 -385-982-336 -690-584-17 -092-508-1 -435-115-1 -098-310-1 -098-310-1 -099-508-15 -099-508-15 -099-508-15	7-206A-1 1-999-5 2-769-13 3-553-10 7-993-10
(EF-2 KINASE	ATACCTGATC	Length 126 Indels		Sequence	Sequence Sequence Sequence Sequence Sequence
8)	3CCAAA 570 3CCAAA 60 3GCATG 630 3GCATG 120	6; 0; Gaps		3; 221 222 231 117 117 121,	1, 13, 10, 10,
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INFORMATION FOR SEQ ID NO: 7:
                      1439 TAGAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTC 1498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CU
                                                                       1901 GTATATTAGGTACCAATCTCTACAGTGGCTCCTATGATAAAACTATAAGAGTTTGGAATT 1960
                                                                                                                                                                                                                   1319 CAAGTACTTGTGAATTTGTAAGGACCTTAAATGGACACAAACGAGGCATTGCCTGTTTGC 1378
                                                                                                                                                                                                                                                                                                                                                                 1730 TGGAATGTAAATATACCCTTGAAAGTCATGCCAGA------GCCGTCAAAACACTTT 1780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2237 base pairs
                                                                                                                                                                                                                                                                   1781 GTATATCTGGTCAATATTTATTTAGTGGTTCAAATGATAAAACTATCAAGGTTTGGGATT 1840
                                                                                                                                                                                                                                                                                                              1259 ACTTTGATGACAAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTATGGAACA 1318
                                                                                                                                                                                                                                                                                                                                                                                                               1199 CAACTGACATTACCCTCCGGAGGGTGCTGGTCGGACACCGAGCTGCTGTCAATGTTGTAG 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1670 ATAAATATTTGTTTAGTGGTTCCTCTGACAAAACTATCAAAGTTTGGGATTTGAAAACTT 1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1079 GTGAAATGCTAAACACGTTGATTCACCATTGTGAAGCAGTTCTGCACTTGCGTTTCAATA 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1550 ATCAATATTTGTTTAGTGGTTCATCAGATCATTCAATTAAAGTTTGGGATTTAAAGAAAT 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1019 AGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGGATGTAAATACAG 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1490 TGGAATGTGTTCAAACCTTGAAAGGTCATGAAGGTCCAGTTGAATCAATTTGTTATAATG 1549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Simhes 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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STREET: 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                    AGTACAGGGACAGGCTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACA 1438
                                                                                                                                                                     TGAAAACTTTTCGTTGTAACTACACTCTAAAAAGGTCATACTAAATGGGTCACCACTATCT 1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGCCATGATGGTGACCTGCTCCAAAGATCGTTCCATTGCTGTATGGGGATATGGCCTCCC 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAAGATGTATTTTACTTTGGAGGGTCATGATAAACCTGTCCATACGGTTCTATTGAATG 1669
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EDNESS: double
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                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                1453 TGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTCGATTTGATAACAAG 1512
                                                             1138 ATACTTGTCACTGGATCACGAGATACCACTCTTCGTGTATGGGACGTAGAATCCGGACGT 1197
                                                                                                                                                                                                                      1018 TATATTGTTAGCGGGTCCACTGATAGAACTGTAAAAGTTTTGGAGTACTGTAGATGGTTCA 1077
                                                                                                                                                                                                                                                            1273 TACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTATGGAACACAAGTACTTGTGAA 1332
                                                                                               1393 CTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACATAGAATGTGGTGCA 1452
                                                                                                                                       1078 CTTCTTCATACACTTCAAGGACATACTTCCACTGTTCGATGCCATGGCTATGGCTGGTTCC 1137
                                                                                                                                                                                1333 TTTGTAAGGACCTTAAATGGACACAAACGAGGCATTGCCTGTTTGCAGTACAGGGACAGG 1392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 24-JU
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STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
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INVENTION: SEL-10 AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2481 base pairs
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US-08-283-917-8
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                                                                                                         Query Match
                                                                        Matches
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 1
FILING DATE: 03-AUG-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: OXIDIZED PHOPHOLITITLE OF INVENTION: AND GENE THEREOF NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1198 CACCTGGCAACTTTACATGGCCATCATGCAGCCGTTCGATGCGTTCAATTCGATGGAACA 1257
                                                                                                                                                                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 03-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5849557man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
1184 TCATTTTCCATCCTGTGTTCAGTGTTATGGTCTCTGCTTCAGAGGATGCTACAATTAAGG 1243
                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 413-3000
                                   1001 TCTGTCTCCAGTATGATGAGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAG 1060
                                                                                                                                                                                                                                                                                         LENGTH: 2085 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: JP 209943/1993 FILING DATE: 03-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: NEUSTADT, P.C.
                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                        Match 2.4%;
Local Similarity 47.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACCCCCGTGCTCCTGCAGG 1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAAGTGTGGGGATCTTGTGGCCTGCTTTG 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTGTTGTTTCGGGAGGATATGATTTTACCGTTAAAATTTGGAATGCTCATACTGGGAGA 1317
                                                                      262;
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ARAI, HIROYUKI
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                                                                                                                                                                                                                                                                             unknown
                                                                        Conservative
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                                                                                                                                                                                                                         Bos taurus
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                                                                                                                                                                                                                                                          CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIDEKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/283,917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2292-030-0
                                                                      Score 50.8; DB 2;
Pred. No. 5.6e-06;
0; Mismatches 277;
                                                                                                       Length 2085;
                                                                      Indels
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; Sequence 8, Application US/08961716
; Patent No. 5880272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: OXIDIZED PHOPHOL TITLE OF INVENTION: AND GENE THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
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                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                     APPLICATION NUMBER: JP 209943/1993
APPLICATION NUMBER: JP 209943/1993
APPLICATION NUMBER: JP 209943/1993
APPLICATION NUMBER: JP 209943/1993
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STATE: Virginia
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                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATAGAACTATAAAGGTATGGAACACAAGTACTTGTGAATTTGTAAGGACCTTAAATGGAC 1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGATATTTCATTCGACCACAGTGGCAAGCTTCTGGCTTCATGTTCTGCAGATATGACCA 1363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATCTGACAACACTATCAGATTATGGGACATAGAATGTGGTGCATGTTTACGAGTGTTAG 1468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGAACATGAGCATGTGGTAGAATGCATTTCCTGGGCTCCTGAAAGCTCATATTCTTCCA 1720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGCTGTATGGGATATGGCCTCCCCAACTGACATTACCCTCCGGAGGGTGCTGGTCGGAC 1234
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Oblon,
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TSUJIMOTO, MASAFUMI
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No.
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5880272man F
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US-08-232-463-14/c
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; LOCATION:
US-08-961-716-8
                Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.4%; Score 50.8; DB 2; Best Local Similarity 47.3%; Pred. No. 5.6e-06; Matches 262; Conservative 0; Mismatches 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                         1721 TCTCTGAAGCAACA 1734
                                                                                                                                                                                                                                                                                                                                                   1469 AAGGCCATGAGGAATTGGTGCGTTGTATTCGATTTGATAACAAGAGGATAGTCAGTGGGG 1528
  APPLICANT:
                                                                                                                                                                                                                                                                    1529 CCTATGATGGAAAA 1542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1121 TGCACTTGCGTTTCAATAATGG-----CATGATGGTGACCTGCTCCAAAGATCGTTCCA 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1061 TGTGGGATGTAAATACAGGTGAAATGCTAAACACGTTGATTCACCATTGTGAAGCAGTTC 1120
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REFERENCE/DOCKET NUMBER: 22:
TELECOMMUNICATION INFORMATION:
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ORIGINAL SOURCE:
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TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
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                                                                                                                                                                                                                                                                                                                                                                                                                                        CATCTGACAACACTATCAGATTATGGGACATAGAATGTGGTGCATGTTTACGAGTGTTAG 1468
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FALKNER, F. G.
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Best Local
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TELEX: 899149
INFORMATION FOR SEQ ID NO:
1088 RRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCCTCGACCTGCAG 1043
                                                                                                                                      REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: EP 9:
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                             946 GATAAAAAACACATTGGAATGCAAGCGAATTCTCACAGGCCATACAG 991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                             766 AGAGCACTTTATCCTAAAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGT 825
                                                                                                                                                                                                                                                                                                                                                                                     646 ATCGAGAGAATGGTCAGGACAGATTCTCTGTGGAGAGGCCTGGCAGAACGAAGAGGATGG 705
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                                                                                                                                                                                                                                                                                                                  706 GGACAGTATTTATTCAAAAACAAACCTCCTGACGGGAATGCTCCTCCCAACTCTTTTTAT 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                              586 GAACTTGTGTGCAAGGAATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTT 645
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                                                                                                      TTACAGTATGATGATCAGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGG 945
                                                                                                                                                                          GGAAGACATAGTTTACAGAGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGT 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Conservative 218; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 2.3%; Score 50; DB 1; Length 7218; Similarity 4.9%; Pred. No. 2.4e-05;
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                                                                                                                                                                                                                                                                                                                       Matches 131;
                                                                                                                                                                                                                                                                                                                                            Best
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FILING DATE: 28-VAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: (415) 781-1989
TELEPAN: (415) 398-3249
TELEEAX: 910 277299
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CURRENT APPLICATION DATA:
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TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
                                                                                                                                                                                                                                        1625 ATTCTAATTATGTTGCTACGGGCTCTGCAGACAGAACTGTGCGGCTCTGGGGACGTCCTGA 1684
                                                                                                                                                                                                                                                                             1265 ATGACAAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTATGGAACACAAGTA 1324
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1805 TTGGACATGGTTTGATGGTTGGAGAATTAAAAGGCCCACACTGATACAGTCTGTTCACTTA 1864
                                                                               1745 CTCCCAATGGGAGATTCCTGGCTACAGGAGCAACAGATGGCAGAGTGCTTCTTTGGGATA 1804
                                                                                                                   1383 ----CAGGGACAGGCTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACA 1438
                                                                                                                                                            1325 CTTGTGAATTTGTAAGGACCTTAAATGGACACAAACGAGGCATTGCCTGTTTGCAGTA-- 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                      Match 2.2%;
Local Similarity 52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: doub
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                                     TAGAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTC 1498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2152 base pairs
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Tanese, Naoko
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                                                                                                                                                                                                                                                                                                                     0; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                          Score 47.8; DB 1; Pred. No. 5.5e-05;
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                                                                                                                                                                      Matches 131;
                                                                                                                                                                                      Query Match 2.2%;
Best Local Similarity 52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIE: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
                                                                                                                                                                                                                                                                                                                                                                        TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2152 base pair
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                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/188,582
APPLICATION NUMBER: US 08/188,582
APPLICATION NUMBER: 28-UNATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
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1383 ----CAGGGACAGGCTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACA 1438
                                  FEATURE:
                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                    1325 CTTGTGAATTTGTAAGGACCTTAAATGGACACAAACGAGGCATTGCCTGTTTGCAGTA-- 1382
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                                                                                                                                                                                                                                                           NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                               TYPE:
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(415) 398-3249
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Weinzierl, Robert O.J.
WEINZION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
VENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
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Tanese, Naoko
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Comai, Lucio
                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                             linear
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09-MAY-1996
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Pred. No. 5.5e-05;
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                                                                                                                                                                                       Query Match
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 304
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                          TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
                                   1774 AGATAAATAACCATACACTGACCTCATACTTGCCCCAGGACCCCATTAAAGTTGCGGTATTT 1833
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DC COMPONS NS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
1714 GATCCAGCTGCCCAAGCTGAACCCCCCCCGTTCCCCCTTCTCGAACATACACCTACATCTCC 1773
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FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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CURRENT APPLICATION DATA:
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APPLICANT: SCHEIFLIGER, F. G.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBIN
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                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                CLONE:
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                                                                                                                                                                     ocal Similarity
                                                                                                                                                                                                                                                                                                                                        ENGTH:
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                                                                                                                                                                                                                                                                                                                                    7218 base pairs
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1800 Diagonal Road, Suite 500
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                                                                                                                                                   Conservative 210;
                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                   1.9%; Score 39.8; DB 3.6%; Pred. No. 0.052;
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                                                                                                                                                   Mismatches
                                                                                                                                                                                     DB 1; Length 7218;
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US-08-664-596B-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
 Query Match 1.8%;
Best Local Similarity 51.4%;
Matches 89; Conservative
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                                                                                                                                                                                                                               NAME: Brown, Scott A.
REGISTA NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
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APPLICANT:
                                                                                        MOLECULE TYPE: CDNA
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                         TOPOLOGY:
                                                                                                                         STRANDEDNESS:
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Bowman, Michael
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Treacy, Maurice
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LaVallie, Edward
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                        double
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Score 38.6; DB 1; Length 433; Pred. No. 0.019; 0; Mismatches 84; Indels
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                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 876-5851 (NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
1516 ATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTGTGGGGATCTTGTGGCTGC 1568
                                                                                                                                              1396 GTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACATAGAATGTGGTGCATGT 1455
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                    1456 TTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTCGATTTGATAACAAGAGG 1515
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                                                      167 CAGGACACGTTAATGGGACATGATGCTGTTAGTAAGATCTGTTGGCATGACAACAGG
                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/738,367
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Treacy, Maurice
Spaulding, Vikki
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McCoy, John
LaVallie, Edward
                                                                                                                                                                                              Conservative
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                                                                                                                                                                                              0;
                                                                                                                                                                                          Score 38.6; DB 1;
Pred. No. 0.019;
0; Mismatches 84;
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US-08-738-367-6
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                                                                                      RESULT 13
US-09-156-425-1
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                                                   Sequence 1, Application US/09156425B Patent No. 5962671
                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
 APPLICANT: Baker, Brenda F APPLICANT: Cowsert, Lex M.
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; MOLECULE TYPE: US-08-738-367-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 876-5851 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617), 498-8224
                                                                                                                                                                                        1396 GTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACATAGAATGTGGTGCATGT 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                    1516 ATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTGTGGGATCTTGTGGCTGC 1568
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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CTTY: Cambridge
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227 CTATATTCTGCATCGTGGGACTCTACAGTGAAGGTGTGGTCTGGTGTTCCTGC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                    Local Similarity
les 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                         CAGGACACGTTAATGGGACATGATGATGCTGTTAGTAAGATCTGTTGGCATGACAACAGG
                                                                                                              TTACGAGTGTTAGAAGGCCCATGAGGAATTGGTGCGTTGTATTCGATTTGATAACAAGAGG 1515
                                                                                                                                                      GTCATAACTTCTTCATGGGATAATAATGTCTATTTTTATTCCATAGCATTTGGAAGACGC 166
                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                              733 base pairs
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VENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
VENTION: ENCODING THEM
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Treacy, Maurice
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; NAME/KEY: CDS
; LOCATION: (13)..(2766)
US-09-156-425-1
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; LOCATION: (18)..(1265)
US-08-965-048-3
US-09-318-448-11
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US-08-965-048-3/c
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                       RESULT 15
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Best Local Similarity 51.4%;
Matches 89; Conservative
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LENGTH: 3380
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Best Local Similarity 56.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chen, Hong
APPLICANT: Freimer, Welson
APPLICANT: Freimer, Nelson
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF NEUROPSYCHIATRIC DISORDERS
FILE REFERENCE: 7853-093
CURRENT EPPLICATION NUMBER: US/08/965,048
CURRENT FILING DATE: 1997-11-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: ANTISENSE MODULATION OF FAN EXPRESSION FILE REFERENCE: RTS-0009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                    1422 TAA 1420
                                                                                                                                                                            1482 ATCTAPACTTATTTAAGGATTAAGTAGGATAACGTGCATTGATTTGCTAAAAGAATCAAG 1423
                                                                                                                                                                                                                                                              2191 CTATATTCTGCATCGTGGGACTCTACAGTGAAGGTGTGGTGTCTGGTGTTCCTGC 2243
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                                                                                                                                870 CAA 872
                                                                                                                                                                                                                  810 ATCTAATTGGAGATGTGGAAGACATAGTTTACAGAGAATTCACTGCCGAAGTGAAACAAG 869
                                                                                                                                                                                                                                                                                                        750 TCCCAACTCTTTTTATAGAGCACTTTATCCTAAAATTATACAAGACATTGAGACAATAGA 809
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Pred. No. 0.077;
0; Mismatches 84; Indels 0
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; ORGANISM: Homo sapiens US-09-318-448-11
Search completed: February 22, 2003, 01:51:48 Job time: 183 secs
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 69; Conserv
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SEQ ID NO 11
LENGTH: 18596
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Johnson, William G.
APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REFERENCE: 601-1-057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
                                                                                                       16904 TAA 16906
                                                                                                                                                                                                              16844 ATCTAAACTTATTTAAGGATTAAGTAGGATAACGTGCATTGATTTGCTAAAAGAATCAAG 16903
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                                                                                                                                                          870 CAA 872
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Listing first 45 summaries
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B48088 beta-transd N,Alternate C;Species: C,Jate: 26- C;Accession R;Spevak, Mol. Cell. A;Title: Sa A;Reference A;Accession A;Status: p A;Residues: ref C;Superfami C;Keywords: F;431-462/U		44444998 54444998
B48088 B48088 B48088 beta-transducin repeat-containing beta-transducin repeat-containing c; Species: Xenopus laevis (Africa C; Date: 26 May-1994 #sequence_rev C; Accession: B48088 C; Caccession: B48088 B; Stratt Mol. Cell. Biol. 13, 4953-4966, 1 A; Title: Saccharomyces cerevisiae A; Reference number: A48088; MUID: A; Accession: B48088 A; Ratus: preliminary A; Molecule type: mRNA A; Residues: 1-518 <spe> A; Cross-references: GB: M98268; NI C; Superfamily: unassigned WD repe C; Keywords: duplication F; 431-462/Domain: WD repeat homol</spe>		330 320 318 313.5 312.5 312.5 312.3 312.3 312.3 306.5 306.5 306.5 299.5 299.5 299.5
ucin repeat-conta p names: beta-Trcp xenopus laevis (A May-1994 #sequenc 13 H4088 4); Keiper, B.D.; Biol. 13, 4953-49 Biol. 13, 4953-49 Ferences: GB:M9826 Eferences: GB:M9826 Ily: unassigned WD comain: WD repeat		100.55 100.33 100.33 100.33 100.11 100.11 100.11 100.11
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ican clawed frog 994 #text_change non, M.J. arrested at a la :8393141 N:AAA02810.1; PII D repeat homology	Ø	probable # WD-40 repe CDC4 repes hypothetic hypothetic hypothet trans WD-40 repeat transcrip apoptotic WD-40 repeat trp-asp re WD-40 rep
g e 21-Jul-2000 late stage in anap lTD:g295543		probable WD-repeat WD-40 repeat prote CDC4 repeat unit-c hypothetical prote hypothetical prote wD-40 repeat protei beta transducin-libeta transducin-libeta protein burnepeat protein wD-repeat protein Transcription init apoptotic protein wD-repeat protein wD-repeat protein wD-repeat protein wD-repeat protein wD-40 repeat wD-40 repeat wD-40 repeat wD-40 repeat wD-40 repeat wD-40 repeat

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Best Local Similarity 198 343 318 223 258 163 43 GTSSMIVPKQRKLSANYEKEKELCVKYFEQWSECDQVEFVEHLISRMCHYQHGHINTYLK 78 GTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLK 137 13 ASEREDCHRDEPPRKIITEKNTLRQ-----TKLAN 42 RVIITGSSDSTYRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMAVTCSKDRSIAVWDMASP RTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSL 257 TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ TDITLRRVLÝGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ 437 RVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASA 342 RTDSLWRGLAERRGWGQYLFKNKPPDGKTPPNSFYRALYPKIIQDIETIESNWRCGRHSL Conservative 85.6%; 91.6%; 7; Mismatches Score 2597; Pred. No. 1. DB 2; Length 518; ..2e-193; es 8; Indels 3 Indels 30; Gaps 402 222 ŗ

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A;Accession: T16607
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #t
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A;Experimental source: strain Bristol N2
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A; Residues: 1-701 <MIL>
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                                                                                                                                                                                                                                                                                                                         DYSCSRILSGHTGSVLCLQYDNRVIISGSSDATVRVWDVETGECIKTLIHHCEAVLHLRF 346
                                                                                                                                                                                                                                                                                                                                               TLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRF 355
                                                                                                                                                                                                                                                                                                                                                                                                                                      YPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGYYCLQYDDQKIVSGLRDNTIKIWDKN 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NVRSDSLWWGLSEKRQWDKFLNISRDMSVRRICEKFNYDVNIKRDKLDQLILMHVFYSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MVRTDSLWRGLAERRGWGQYL-----
                                                                                               IRFDEKRIVSGAYDGKIKVWDLQAALDPRALSSEICLCSLVQHTGRVFRLQFDDFQIVSS
                                                                                                                                                                                                                                                                                                                                                                                                    YPKIIRDIHNIDNNWKRGNYKMTRINCQSENSKGVYCLQYDDDKIVSGLRDNTIKIWDRK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFLFPSRNTQIFLSYSRSFSSFSEVL----KWSEHEQLDFMDKIVHRLSHYQLGKVDNF 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.9%; Score 1635.5; DB 2; Length 701; 57.7%; Pred. No. 8.1e-119; tive 69; Mismatches 116; Indels 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----FKNKPPDGNAPPNSFYRAL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55;
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                         R;Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, April 1997
                                                                               probable sulfur metabolite control protein - fission yeast (Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 26-May-2000
A; Reference number: A; Accession: T38932
                                                                         C; Accession: T38932
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RESULT 4
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A;Map position: 1
A;Introns: 43/1; 74/3
C;Superfamily: unassigned WD repeat proteins; WD repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-506 <MCD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K;MCDOugall, R.C.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Murphy, L.; Jones, L.; submitted to the EMBL Data Library, January 2000
A; Reference number: Z25046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain 972h(-);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:AL136538; PIDN:CAB66464.1; GSPDB:GN00066; SPDB:SPAC30.05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: T50211
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Best Local
                                                                              456
                                                                                                                498 VAALDPRAPAGTICLRTLVEH-----SGRVFRLQFDEFQIVSSSHDDTILIWDF 546
                                                                                                                                                                                                                                                                                                                             380
                                                                                                                                                                                                                                                                                                                                                                                                              322 TGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVW--DMASPTD 379
                                                                                                                                                                                                                                                                                                                                                                              278
                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 RATIDSVYCVQYDDEIMVSGSKDRTVSVWDVNSRFILYKLYGHSGSVLCLDFCRRRNLLV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 LEDPGIWKALYMQKGWFVNENVLNEFEAWRRTHKFPQPRFENFLKQQNIIGPYGTMFLPQ 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 QMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 TSDGMLWKKLI------ERMVRTDSLWRG------LAERRGWG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 ENCVAK----TKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLIS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 KNVVSKVSDLTSCSDFSTSSPVPCLNPLS-----
                                                                                                                                                                                                                                                                ACM-HVLRGHLASVNSVQYSSKTGLIVTASSDRTLRTWDITTGHCIRIIHAHQRGIACAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QFIF-----DSNGRPLLNWSYLY----KEHAHLDSNWRHGRFLVSTFNNPSIRFPADQDF 217
                                                                                                                                                                  YNGKFIVSGSSDLTIRIFEASSGKLLRMLQGHEDLIRTVRFNDEKIVSGGYDGTVRIWN-
                                                                                                                                                                                                              YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL 497
                                                                                                                                                                                                                                                                                                  SGSSDSTITIWDWQNRRPLKVYFGHTDNVLGVVVSENYIISSSRDHTARVWRLDATSPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -ETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDER--VII 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLSKEGVVAVYNHVRSLLFTDFTEVFP----EEVSLRVFSYLDQLDLCKCKLMSKRWKRL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163;
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                                                                    ----FNTGEQHCVLHNSRNSRVFGLQFDHRRIIACTHSSEILVWNF 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.7%; Score 690; DB 2; 30.4%; Pred. No. 1.3e-45;
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Z21818

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-605 <BAD>
A;Residues: 1-605 <BAD>
A;Cross-references: EMBL:E34864; PIDN:CAB08168.1; GSPDB:GN00066; SPDB:SPAC57A10.05c
A;Experimental source: strain 972h-; cosmid c57A10
C;Genetics:
                                                                                                                          A;Molecule type: DNA
A;Residues: 1-640 <ODE>
A;Residues: 1-640 <ODE>
A;Cross-references: GB:Z47047; EMBL:Z46861; NID:g603997; PID:g763300; MIPS:YIL046w R;Thomas, D.; Cherest, H.; Barbey, R.; Surdin-Kerjan, Y.
submitted to the EMBL Data Library, December 1993
                                                                                                                                                                                                                                                                                                                                                     MET30 protein - yeast (Saccharomyces cerevisiae) x,Alternate names: protein Y1905.02; protein Y1L046w C;Species: Saccharomyces cerevisiae C;Date: 28-May 1993 #sequence_revision 24-Feb-1995 #tv
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A;Map position: 1
C;Superfamily: unassigned WD repeat proteins; WD repeat homology
A;Cross-references: EMBL:L26505; NID:g432493; PID:g432494 C;Genetics:
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                                         A; Molecule type: DNA
A; Residues: 1-60, 'I', 62-640 <THO>
                                                                                     A; Reference number: $43750
A; Accession: $43750
                                                                                                                                                                                                                                             A; Reference number: S49931
A; Accession: S49932
                                                                                                                                                                                                                                                                                                           C; Accession: $49932; $43750 R; Odell, C.; Bowman, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASPTDITLRRVLVGHRAAVNVVDF - - DDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---CRQVVLSGHSDGVMCLQLVRNILASGSYDATIRLWNLATFQQVALLEGHSSGVTCLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIHCR----SETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYPTSSNEETISSVKPPSPNSDSKFFLPFKTRPWKEVYAERCR----VECNWRHGR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSM----HNELSGLSEKSRQRVEAVWAAFSEASCSERKLALQGILNNCSSSLLSFASSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VQSLALADSRLFSCSLDGTIKQWDIEKKKCVHTLFGHIEGVWEIAADHLRLISGAHDGVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IACLOYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKI 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FDQCKLISGSMDKTIRIWNYRTSECISILHGHTDSVLCLTFDSTLLVSGSADCTVKLWHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INRK-----CEKCGWGLPLLERNTLYAAKASIQKRYERLTKRGVDQAHESSPVKKAKLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VRTDSLWRGLAERRGWGQYLFKN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----CVHTLKNHSEPVTSVALGDCEVVSGSEDGKIYLWLFNNAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.5%;
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                                                                                                                                                                                                                                                                                         December 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                       24-Feb-1995 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 605;
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C;Superfamily: unassigned WD repeat proteins;
F;298-329/Domain: WD repeat homology <WD1>
F;338-369/Domain: WD repeat homology <WD2>
                                                                                                                                       R;Kumar, A.; Paietta, J.V.
Proc. Natl. Acad. Sci. U.S.A. 92, 3343-3347, 1995
A;Title: The sulfur controller-2 negative regulate
A;Reference number: Z23121; MUID:95241499; PMID:77
A;Accession: T46660
                                                                                                                                                                                                                                              C;Species: Neurospora crassa
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000
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A;Cross-references: SGD:S0001308; MIPS:YIL046w
A; Map position:
A; Introns: 75/3;
                                                                                      A; Molecule type: DNA
A; Residues: 1-650 < KUM>
                                                                                                                                                                                                                               C; Accession: T46660
                                                                                                                                                                                                                                                                               sulfur controller-2 protein [imported] - Neurospora crassa
                                                                                                                                                                                                                                                                                                     T46660
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                                  A; Gene: scon-2
                                                                     A;Cross-references: EMBL:U17251;
                                                                                                                       A; Status: preliminary;
                                                     Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRGIACLQYRD--RLVVSGSS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FDDRKLITGSLDKTIRVWNYITGECISTYRGHSDSVLSVDSYQKVIVSGSADKTVKVWHV
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                                                                                                                                                                                                                                                                                                                                                                                                        RAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTI 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----DNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESRTCYTLR----GHTEWVNCVKLHPKSFSCFSCSDDTTIRMWDIRTNSCLKVFRGHVGQ 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQKIIPLTIKDVENLATDNTSDGSSPQDDPTMTDGADESDTPSNEQETVLDENIPYPTHL
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                                                                   NID:g806757; PIDN:AAA68968.1; PID:g806758
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Pred. No. 3.2e-34;
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PMID:7724564
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encode

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C;Function:
A;Description: negatively regulates sulfur structural gene expression
A;Note: scon-2+ expression is dependent on CYS3 function and the binding of CYS3 to the
C;Superfamily: unassigned WD repeat proteins; WD repeat homology
                                                                                                      A; Map position:
A; Introns: 22/3;
                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                            submitted to the RMBL Data Library, September 1996
A;Reference number: Z19602
A;Accession: T22703
                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F55B12.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22703
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                                                                                                                                                          A; Gene:
                                                                                                                                                                                                      A;Cross-references: EMBL:Z79757; PIDN:CAB02129.1; GSPDB:GN00023; CESP:F55B12.3
A;Experimental source: clone F55B12
                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-579 <WIL>
                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
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       Matches
                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 VY----RDRWQVSYNWKNSRYKLSVL---KGHENGVTCLQLDDNILATGSYDTTIKIWNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 LYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDK 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGT 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV--VDFDDKYIVSASGDRTI 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QRWRTLADSDAVWVRMCEQHVNRK-----CTKCGWGLPLLERKKLRNYTRQRQLAKGGP 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQGILSQLCFPQLSFVSREVNEALKIDFISALPV----ELAQKVLCYLDTVSLTKAAQVS 154
          150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLWDLDTRQVIRTYEGHVGHVQQVLILPPEYEPDEEVLNGASQDNQDAMSVSSGGSGSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FDGHLLASGSSDKTVKIFDFNSKETYCLK----GHSDWVNSTHVDIKSRTVFSASDDTTI 437
                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                               45/2; 77/3; 122/3; 171/2; 211/2; 342/2; 417/3; 478/3; 526/1
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
17.1%; Score 520; DB 2; Length 579; 28.8%; Pred. No. 2.4e-32; tive 78; Mismatches 222; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.5%; Score 531.5; 25.0%; Pred. No. 3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .5; DB 2;
3.6e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -ACLQYRDRLVVS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 650;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---GSSD 449
     70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -PRSG 608
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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  17;
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                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical trp-asp repeat-containing protein - fission yeast (Schizosaccharomyces p C;Species: Schizosaccharomyces pombe C;Date: 12-Feb-1998 *sequence_revision 20-Feb-1998 *text_change 26-May-2000 C;Accession: T38502; 862507 C;Accession: T38502; 862507 R;Jones, L.; Murphy, L.; McNeil, A.; Simpson, I.; Harris, D.; Barrell, B.G.; Rajandre submitted to the EMBL Data Library, October 1995
  밁
                                              Qy
                                                                                               Db
                                                                                                                                                                                                B
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C; Superfamily: unassigned WD repeat proteins; WD
F;18-51/Domain: WD repeat homology <WD1>
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                                                                                                                                                                                                                                                                                                                                                                                       F;104-137/Domain: WD repeat homology <WD2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-267 <J02>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: Z21798
A; Accession: T38502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
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                                                                                                                                                                                                                                                                                                  Matches
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  120
                                         402 --YIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   507
                                                                                                                                                                                                                                            286 DNTIKIWDKNTLECKRILTGHTGSVLCLQYDER--VIITGSSDSTVRVWDVNTGEMLNTL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             484 EGT-CVHMLSGHRSAITSLQWFGRNMVATSSDDGTVKLWD 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              432 TSIRVWDFTRPEGQECVALLQGHTSLTSGMQLRGNILVSCNADSHVRVWDI------H 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       450 NTIRLWDI---ECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAP 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372 AVRCVQFDGTTVVSGGYDFTVKIWNAHTGRCIRTLTGHNNRVYSLLFESERSIVCSGSLD 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       392 AVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDR--LVVSGSSD 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 WDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 QYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE--RVIITGSSDSTVRV 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 CDLNVHRFLKLQKFGDIFERAADKSRYLRADKIEKNWNANPIMGSAV-LRGHEDHVITCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 SKNWKLISEIDKIWKSLGVEEFKHHPDPTDRVTGAWQGTAIAAG-----VTIPDHIQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 CKEWYRVTSDGMLWKKL-IERMV-----RTDSLWRGLAERRGWGQYLFKNKPPDGNAP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 PN-SFYRALYPKIIQDI------ETIESNWRCGRHSLQRIHCRSETSKGVYCL 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 FVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELV 175
                                                                                            61 FGHTDNVLGVVVSENYIISSSRDHTARVWRLDATSPAEACM-HVLRGHLASVNSVQYSSK 119
                                                                                                                                                                                           1 DRTYSYWDYNSRFILYKLYGHSGSYLCLDFCRRRNLLYSGSSDSTIIIWDWQNRRPLKYY 60
                                                                                                                                                                                                                                                                                                                    Local
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TGLIVTASSDRTLRTWDITTGHCIRIIHAHQRGIACAQYNGKFIVSGSSDLTIRIFEASS 179
                                                                                                                                          IHHCEAVLHLRENNGMMVTCSKDRSIAVW--DMASPTDITLRRVLVGHRAAVNVVDFDDK 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WSTVDGSLLHTLQGHTSTVRCMAMAGSILVTGSRDTTLRVWDVESGRHLA---TLHGHHA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QIHDDVLVTGSDDNTLKVWCIDKGEVMYTLVGHTGGVWTSQISQCGRYIVSGSTDRTVKV 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTLCLRTLYEHSGRVFRLQ-FDEFQIVSSSHDDTILIWD 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFTRLLQESNMTNIRQLRAIIEPHFQRDFLSCLPV----ELGMKILHNLTGYDLLKVAQV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESSYSNGSSSSYNADKLSSSRPLQHKLDLSASPSRNNDLNPRVEHLIALFKDLSSAEQMD 86
                                                                                                                                                                                                                                                                                                104;
                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                        17.1%; Score 519.5; 38.0%; Pred. No. 8.8 ative 58; Mismatches
                                                                                                                                                                                                                                                                                                                  8.8e-33,
                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat homology
                                                                                                                                                                                                                                                                                             83;
                                                                                                                                                                                                                                                                                                                                         Length 267;
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                                                        Gaps
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C;Accession: T18521
R;Saupe, S.; Turcq, B.; Begueret, J.
Gene 162, 135-139, 1995
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C;Species: Podospora anserina
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
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A;Molecule type: DNA
A;Residues: 1-1356 <SAU>
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                   1090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     460 GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEH- 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        641 LVFPTGIEDVSYIIFWRSLNVMSQKLRRDIYCLNAPGFLIDNVRVPDPDPLATVRYSCIY 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               581 EMPDDVSDDPESLEEIVKLCGSFLIIRERTVYFVHQSAKDFLLGTASDKASNKASQEAFE 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              701 WIDHLRDLVSSTSSKWVHLLQDDGDIHRFLTTKYLYWLEALSLLRALP-EGINAIRQLES
                                                                                                                                                                                                                              973 VAFSPDGQRVASGSGDKTIKIWDTASG---TCTQTLEGHGGSVWSVAFSPDGQRVASGSD 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 MIVPK------QRKLSASYEKEKE--LCVKYFEQWSESDQVEFVEHL--ISQMCHY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 EPPRKIIPEKNSLRQTYNSCAR-LCLNQETVCLASTAMK-----TENCVAKTKLANGTSS
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                                                                                                                                                                                                                                                                                                                                                                                    NTLECKRILTGHTGSVLCLQY--DERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLH 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKNKPPDGNAPPNSFYRALY----PKIIQDIETIESNWRCGRHSL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLGHTIRGRLIA---IVRDGYRF---ALSYRMIIEKAPLQAYTSAL------V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QHGHINSYLKP-----MLQRD-----FIT------ALPARGLDHI--AEN 159
                                                                                                                                                                                                                                                                                                                                     ASGTCTQTLEGHGGRVQSVAFSPDGQRVASGSDDHTIKIWDAASGTCTQTLEGHGSSVLS 972
                                                                                                                                                                                                                                                                                                                                                                                                                                         GQRVASGSDDKTIKIWDTASGTGTQTLEGHGGSVWSVAFSPDRERVASGSDDKTIKIWDA 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -QRIHCRS----ETSKG-------YYCLQY--DDQKIVSGLRDNTIKIWDK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F-----APTDSMIKKIFKKEEPGWISTISVVEAEWNACTOTLEGHGSSVLSVAFSAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIER----MVRTDSLWRGLAERRGWGQYL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tch 15.0%; Score 455.5; DB 2; al Similarity 26.0%; Pred. No. 8.2e-27; 164; Conservative 102; Mismatches 220;
                                                                                                                                                                      DRTIKVWNTSTCEFVRTLNGHKRGIACLQYR--DRLVVSGSSDNTIRLWDIECGACLRVL 466
                                                                                                                                                                                                                                                                                   LRFN-NGMMVTC-SKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDF--DDKYIVSASG 408
                   EGHGDSVWSVAFSPDGQRVASGSIDGTIKIWD------AASGT-CTQTLEGHGGWVHS 1140
                                                                     EGHEELVRCIRF - - DNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFR 524
                                                                                                                       DKTIKIWDTASGTCTQTLEGHGGWVQSVVFSPDGQRVASGSDDHTIKIWDAVSGTCTQTL 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 145; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----FNTGEQHC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        852
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A; Description: Fission yeast WD repeat protein Popl
A; Reference number: Z22925
A; Accession: T45136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WD repeat protein popl [imported] - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000 C;Accession: T45136; T40157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
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A;Experimental source: strain 972h-; cosmid c2G2
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:y08391; PIDN:CAA69671.1
A;Experimental source: strain h- 972
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C. submitted to the EMBL Data Library, March 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-775 < KOM>
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A; Note: pop1+
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A; Residues: 1-775 <WOO>
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A; Accession: T40157
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                           417
                                                                                                                                                                                                                                                                                                                                                                                                  357 DSKIRTMCLEQSLSA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                               194 ERMYRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 ITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYR-VTSDGMLWKKL------I 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 TFSLDAPNNSVNYSYFSPNLLGNDSKTRQSFPPHSSSSSHNSLHEPVIYDFSSENPSIHP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 REKCLKRRNSSLSSNLHANKRFLFNSQSDGNKKNETFPSTNYSNVFYPNNCDSKEVASET 180
                                                                                                                               371 VWDMASPTDITLRRVLYGHRAAVNVVDFDDKYIVSASGDRTIKVWN------
                                                                                                                                                                                                                                      311 LCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIA 370
                                                                                                                                                                                                                                                                                                                                             254 RHSLQRIHCRSETSKGVYC---LQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSV 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57
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                                                                                                                                                                                    WTFEYVGDTLVTGSTDRTVRVWDLRTGECKQVFYGHTSTIRCIKIVQGNQSTTDTD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTGFPA----EITNLVLTHLDAPSLCAVSQVSHHWYKLVSSNEELWKSLFLKDGFFWDSI 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNHLSSQKNAVLKLAQLISSFEKLPESVRQYLLFHLLSRCGKHAVQNIHKILLPIFQKNF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SYEKEKEL----CVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDF 144
                                                                                                                                                                                                                                                                                           LHAPEKIKRCSFPIHGVRLITKLQFDDDKIIVSTCSPRINIYDTKTGVLIRSLEEHEGDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162;
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                                                                             -DYEKE-----NRPASNDANSMPPYIISSSRDCTIRLWSLPCLDDPPFVNVNE 552
--TSTCEFVRTLNGHK---RGIACLQYRDRLVVSGSSDNTIRLWDIECGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.9%; Score 453; DB 2; 25.8%; Pred. No. 5.8e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86;
                                                                                                                                                                                                                                                                                                                                                                                                        ------ 389
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DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;MoLecule type: DNA
A;Residues: 1-1227 KUR>
A;Cross-references: GB:BA000019; PIDN:BAB77553.1; PID:g17135007; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AE1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguci
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Nostoc sp.
       503 PRAPAGTLCLRTLVEHSGRVFRLQF--DEFQIVSSSHDDTILIWDFL 547
                                                  791 SSGEDSTVRLWDVKTGQCWQIFEGHSKKVYSVRFSPDGQTLASCGEDRSIKLWDIQRG-- 848
                                                                                                                                                                                             393 VNVVDF----DDK--YIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYR--DRLVV 444
                                                                                                                                                                                                                                           674 HTGECLKTLSKNTNKYYSVAFSPDGRILASASQDQTIKLWDIATG---NCQQTLIGHDDW 730
                                                                                                                                                                                                                                                                                                                                           614 GKYFATGLMNGEIRLWQTSDNKQLRIYKGHTAWVWAFAFSPDSRMLASGSADSTIKLWDV 673
                                                                                                                                                                                                                                                                                                                                                                                                                                      554 KIPDESPIDLSGRDFSGLTIWQAYFKEVKLKETIFANSDLTGSVFTETMSSVVSVKFSPD 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 IIQDIETIESN-------WRCGRHSL---QRIHCRS-----ETSKGVYCLQY--D 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPN--SFYRALYPK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           479 -----INTY--PLMK-----ARSLDYI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELYCKEWY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              432 EKASSTQGEKEAESSKFGLESVVM---EYITAKFIENS-----LEEFSQTKKLDF---- 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            378 EKKVMYSLGANREYVSFRELKDDWLTTESPIKVMEALESLLR-----RSLIEKASPTLI 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              463 LRVLEGHEELVRCIRFDNKR--IVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSG 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 EKALKEMNSSERE-----DCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     521 RVFRLQFDEFQIVSSS--HDDTILIWD 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        610 LHVLRGHVGRVYSVTINPSRQQCISAGTDAKIRIWNL----
                                                                                                SGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF--DNKRIVSGAYDGKIKVWDLVAALD 502
                                                                                                                                                VWSVTFSPVTDDRPLLLASSSADQHIKLWDVATGKCLKTLKGHTREVHSVSFSPDGQTLA 790
                                                                                                                                                                                                                                                                                             NTGEMLNTLIHHCEAVLHLRF--NNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAA 392
                                                                                                                                                                                                                                                                                                                                                                                        DQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQY--DERVIITGSSDSTVRVWDV 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RQIQERLILEPVKQKLLNIFGTELELHLRRMLGTLQKEPLPKKGYAAGNLINLLRQLQLD 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.6%; Score 413.5; DB 2 23.9%; Pred. No. 1.3e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
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γQ
                                                     밁
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                                                                                                                                                                                                                                                                                      QΥ
                                                                                                                                                                                                                                                                                                                                        DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;628-659/Domain: WD repeat homology <WD2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: initiation of DNA replication; C; Superfamily: unassigned WD repeat proteins; C; Keywords: cell cycle control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;459-494/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 6L
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-779 < MUW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: S62304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, April 1994 A; Reference number: S62302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-459, 'E', 461-779 < YOC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: SGD:S0001885; MIPS:YFL009w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: SGD: CDC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Murakami,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A: Residues: 1-579 <CHU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, September 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-779 < MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: protein YFL009w C;Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S48310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Churcher,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ъ
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rest
                                                                                                                                     295 IINSLGVSQNWNKIIRKSTSLWKKLLISENFV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        849 -----ECVNTLWGHSSQVWAIAFSPDGRTLISCSDDQTARLWDVI 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 13.2%;
Similarity 24.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S56245
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S48310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat homology <WD1>
                                                                                                                                                                                                                                                                                                                                                                                                                              80; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 399; DB 2;
Pred. No. 9.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                           196;
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R:Yoohem, J.; Byers, B.

J. Mol. Biol. 195, 233-245, 1987

A:Title: Structural comparison of the yeast cell division cycle gene CDC4 and a relat A; A; Reference number: A26867; MUID:88011240; PMID:3309335

A; Accession: A26867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:D31600; NID:g836814; PIDN:BAA06495.1; PID:d1007066; PID:g836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X05625; NID:g3502; PIDN:CAA29113.1; PID:g3503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sas submitted to the EMBL Data Library, May 1995
A;Description: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces A;Reference number: S56186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:Z46255; NID:g559925; PIDN:CAA86341.1; PID:g559926; MIPS:YFL0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:D50617; NID:g836685; PIDN:BAA09229.1; PID:d1009870; PID:g836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 02-Sep-1995 #sequence_revision 12-Apr-1996 #text_change 26-May-2000 C;Accession: 856245; 848310; A26867; 862304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell division control protein CDC4 - yeast (Saccharomyces cerevisiae)
277 DQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE-RVIITGSSDSTVRVWDVN 335
                                                                              332 NSLNLKLSQKYPKLSQQDRLRLSFLENIFILKNWYNPKFVPQRTTLRGHMTSVITCLQFE 391
                                                                                                                                                        226 APPNSFYRALYPKIIQD-----IET--IESNWRCGRHSLQRIHCRSETSKGVYCLQYD 276
                                                                                                                                                                                                                                                                                                            169 LCAAELVCKEWYR-VTSDGMLWKKLI--ERMVRTDSLWRGLAERRGWGQYLFKNKPPDGN 225
                                                                                                                                                                                                                                                                                                                                                                                          245 -----EISLKIFNYLQFED 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 TTPLAKTIKTINN------NNNIADLIESKDSIISPEYLSDEIFSAINNNLPHAYFK-- 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 SESDQVEFVEHLISOMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 TVCLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEK-----ELCVKYFEQW 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              separation of the spindle pole bodies t WD repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 156;
                                                                                                                                                                                                                                      ----SPKGF 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
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;Cross-ref;Genetic,Gene: pop;Gene: pop;Hap posit;Function;Descripti;Quescripti;Quescripti;Quescripti;Quescripti;Quescripti;Query Mat Loca Matches	RyGentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. RyGentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, August 1996 A; Reference number: Z1812 A; Accession: T38794 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-703 <gen- 1-703="" 1998="" 8159-8164,="" 95,="" 972h-;="" <jal="" a;="" acad.="" accession:="" and="" c4d7="" cdc18="" cosmid="" cross-references:="" cyclin-dependent="" d.;="" ddbj="" embl="" embl:z98602;="" experimental="" fd="" from="" gb="" gspdb:gn00066;="" jallepalli,="" kelly,="" kinase-phosphorylated="" muid:98318628;="" natl.="" number:="" p.v.;="" pidn:cab11275.1;="" pmid:9633157="" preliminary;="" proc.="" proteins="" r;="" reference="" residues:="" rum1="" sci.="" source:="" spdb:spac4d7.03="" status:="" strain="" sudl+="" t.j.="" t43798="" targets="" tien,="" title:="" translated="" u.s.a.="" z22686;=""></gen->	RESULT 13 743557 F-box/WD-repeat protein pop2 - fission yeast (Schizosaccharomyces pombe) N.Alternate names: proteolysis factor sudlp C;Species: Schizosaccharomyces pombe C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000 C;Accession: T43557; T38794; T43798 R;Wolf, D.A.; Jackson, P.K. submitted to the EMBL Data Library, December 1997 A;Description: Fission yeast pop2 encodes a novel F-box/WD-repeat protein involved in the A;Reference number: Z22576 A;Accession: T43557 A;Accession: T43557 A;Accession: T43557 A;Residues: 1-703 <wol> A;Residues: 1-703 <wol> A;Cross-references: EMBLAF038867; PIDN:AAB95480.1 A;Cross-references: EMBLAF038867; PIDN:AAB95480.1</wol></wol>	Db 392 DNYVITGADDKMIRVYDSINKKFLLQLSGHDGGVWALKYAHGGILVSGSTDRTVRVWDIK 451 Qy 336 TGEMLNTLIHHCEAVLHLRENNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV 395
	RESULT 14 A12493 A12493 WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha C;Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: A12493 R;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001 A.;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:1173567: Gephs.GNO180 A;Accession: A12493 A,Sctatus: preliminary A;Molecule type: DNA A;Coross-references: GR-RA000020. DIDN.BAB73013 1. DID:G17135667: Gephs.GN0180 A. COROSS-references: GR-RA000020. DIDN.BAB73013 1. DID:G17135667: Gephs.GN0180	Qy 341 NTLIHHCEAVLHLRENNGMMYTCSKDRSIAVMDMASPTDITLRRVLVGHRAAVNVVDFDD 400 473	Qy 60 ASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEK-EKELCVKYFEQWSESDQVEFVE 118

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A:Molecule type: DNA
A:Residues: 1-1747 <KUR>
A:Residues: 1-1740 <KUR>
A:Cross-references: GB:BA000019; PIDN:BAB77807.1; PID:g17135261; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: a110283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC1842
A;Status: preliminary
Search completed: February 20, 2003, 09:55:48 Job time: 28 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Nostoc sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
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                                                                                                                     1721 QQGCDRITDYLQHNSNV 1737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1547 VNDGQLLRTLTGHNDEVTSVNFSPDGQFLASGSTDNTVKIWQ----TDGRLIKNITGHGL 1602
                                                                                                                                                                                                                                     1663 ADNTIKLWNLPNATLLKTLLGHPGKINTLAFSPDGKTLLSGGEDAGVMVWNL--DLDDLM 1720
                                                                                                                                                                                                                                                                                                                                                     1603 AIASVKFSPDSHTLASASWDNTIKLWQVTDGKLINNLNGHIDGVTSLSFSPDGEILASGS 1662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1487 DGKTIATASADNTIKLWDSQTQQLIKTLTGHKDRITTLSFHPDNQTIASGSADKTIKIWR 1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1045 NQYLATGGDDSVVRLWDIGKGVCVRTFSGHTSQVICILFTKDGRRMISSSSDRTIKIWN 1103
                                                                                                                                                                                                                                                                       448 SDNTIRLWDIECGACLRVLEGHEELVRCIRF--DNKRIVSGAYDGKIKVWDLVAALDPRA 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 DDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQY--DERVIITGSSDSTVRVWD 333
                                                                                                                                                                             506 PAGTLCLRTLVEHSGRV 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334 VNTGEMLNTLIHHCEAVLHLRF -- NNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        985 QTLQGHPGSVLAVAFSCDGKTLFSSGYEKLVKQWDVETGYCLQTWEADSNRVWAVAVSRD 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    464 RVLEGHEELVRCIRF--DNKRIVSGAYDGKIKVWDL--------VAALDP 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           406 ASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYR--DRLVVSGSSDNTIRLWDIECGACL 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           865 NWEHSLLASGHEDQTIKLWDLNLHSPHKSNVNTHPFRILQGHSNRVFSVVFSSTGQLLAS 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 --- NGMMVTCSKDRSIAVWD--MASPTDITLR----RVLVGHRAAVNVVDEDD--KYIVS 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            925 GSADRTIKLWSPHTGQCLHTLHGHGSWVWAIAFSLDDKLLASGSYDHTVKIWDVSSGQCL 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              805 RCLDTLKKHTNRIWSVAFHPQGHLFVSGGDDHAAKIWELGTGQCIKTFQGHSNATYTIAH 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   AVNVVDF--DDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYR--DRLVVSGS 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.4%; Score 375; DB 2; Length 1747; 32.7%; Pred. No. 2.1e-20; tive 50; Mismatches 107; Indels 16;
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Database :
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                           GenEmbl:*
1: gb_ba:*
2: gb_htg:
3: gb_in:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1740	GATGACACAATCCTCATCTGGGACTTCCTAAATGATCCAGCTGCCCAAGCTGAACCCCCC	S	Qy	
1680	TTCCGGAAG	1621	Дb	
1680	ATTCCGGAAGAGTTTTTCGACTACAGTTTGATGAATTCCAGATTGTCAGTAGTTCACAT	1621	Qy	
62	GTGGCTGCTTTGGACCCCCGTGCTCCTGCAGGGACACTCTGTCTACGGACCCTTGTGGAG	1561	Дb	
	TGGCTGCTTTGGACCCCCGTGCTCCTGCAGGGACACTCTGTCTACGGACCCTTGTGGAG		Qy	
1560 1560	TTTGATAACAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTGTGGGATCTT	1501	Db .5	
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0	GAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTCGA	1441	P 04	
4	TACAGGGACAGGCTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACATA	1381	₽ B	
1440	ACAGGGACAGGCTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACA	σ	Qy	
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32	TTGATGACAAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTATGGA	2	Qy	
26	ACTGACATTACCCTCCGGAGGGTGCTGGTCGGACACCGAGCTGCTGAATGTTGTAGAC	1201	Db	
26	ATTACCCTCCGGAGGGTGCTGGTCGGACACCGAGCTGCTGTCAATGTT0		Qy	
20	GCATGATGGTGACCTCCTCCAAAGATCGTTCCATTGCTGTATGGGATATGGCCTCCCCA	1141	рь	
20	GGCATGATGGTGACCTGCTCCAAAGATCGTTCCATTGCTGTATGGGATATGGCC	-	Qy	
4	GAAATGCTAAACACGTTGATTCACCATTGTGAAGCAGTTCTGCACTTGCGTTTCAATAAT	1081	Db	
_	AAATGCTAAACACGTTGATTCACCATTGTGAAGCAGTTCTGCACTTGCGTTT	1081	Ωу	
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2 2	AGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGATGTAAAT		Qy	
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3 6	GAATGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCCTCTCTCT		Qy	
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900	CASAGAATTICACTISCCGAAGTGAAACAAGCAAAGGAGTTTACTGTTTACAGTATGATGAT	841	β ζ	
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840	1 AAAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGTGGGAAGACATAGTTTA	78:	Qy	
780	ACAAACCTCCTGACG	721	Db	
780	CAAACCTCCTGACGGGAATGCTCCTCCCAACTCTTTTTATAGAGCACTTTATCC	N	γQ	
	AGGACAGATTCTCTGTGGAGAGGCCTGGCAGAACGAAGGATGGGGACAGTATTTATT	661	Дb	
72	GACAGATTCTCTGTGGAGAGGCCTGGCAGAACGAAGGATGGGGACAGTATTTA	on .	Qy	•
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Sequence 42 from Patent WO0075184.
AX057166
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Zhang, H., Tsvetkov, L.M. and Kondo, T.
Modulation of protein levels using the
Patent: WO 0075184-A 42 14-DEC-2000;
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Cenciarelli, C., Chiaur, D.S., Guardavaccaro, D., Parks, W., Vidal, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="F-box protein Fbw1A"
/protein_id="AAF04464.1"
/db_xref="GI:6164610"
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70. .1779
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                        Submitted (03-JUL-1997) R. Be Interactions Proteigues, CHU
                                                                                                                                    Margottin, F., Bour, S.P., Durand, H., Selig, L., Benichou, S., Richard, V., Thomas, D., Strebel, K. and Benarous, R. A novel human WD protein, h-beta TrCp, that interacts with Ypu connects CD4 to the ER degradation pathway through an motification.
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                       Akhter, N. Ayele, K. Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Birinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                      Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                           Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                   Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                  608 CATATTGCTGAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTT
                                                                                                                                                                                                 532 CATATCGCTGAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTT
                                                                                                                                                                                                                                                                           548 TATCTTAAACCTATGTTGCAGAGAGATTTCATAACTGCTCTGCCAGCTCGGGGATTGGAT
           652 AGAATGGTCAGGACAGATTCTCTGTGGAGAGGCCTGGCAGAACGAAGAGGATGGGGACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAGAGAAGAATTCACTTAGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCCAGAATTCCTCAGAGAGAGAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAAAGGAAAAGGAACTGTGTGAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAAAGGAAAAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTG
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                                                                                                                                                                                                                                                                                                                                                                               GAATTTGTGGAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTGCCAATGGCACTTCCAGTATGATTGTGCCCCAAGCAACGGAAACTCTCAGCAAGCTAT 351
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4502476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MDDAEAVLQEKALKFMCSMPRSLWLGCSSLADSMPSLRCLYNPG
TGALTAFQNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLHQETVCLASTAMKT
ENCVAKTKLANCTSSM YPKQRKLSASY EKEKELCVKY FEQWSESDQVEFVEHLISQM
CHYQHGHINSYLKPMLQRDFITALPARGLDHAENLISYLDAKSLCAAELVCKEWTYV
TSDGMLMKKLIEEMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII
QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKINDKNTLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ÖKRILTGHTGSVLCLQYDERVIITGSSDSTVRVMDVNTGEMLMTLIHGCEAVLHILREN
NGMMYTCSKDRSIAKVMDMASPTDITLRRYLVGHRAAVNVDFDDKYIVASGDRTIKV
WNTSTCEFVERTLNGHRGIACLQYRDBLVVSGSDNTIRLMDLECGACLRAVLEGHEEL
VRCIRFDNKRIVSGAYDGKIKVMDLYAALDPRAPAGTLCLKTLVEHSGRVFRLQFDEF
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/clone_lib="NHLMGC_115"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="MGC:40028 IMAGE:5180993"
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/db_xref="LocusID:8945"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="beta-transducin repeat containing"
/protein_id="AAH27994.1"
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                                                                                                                                                                                                                        TGGGATCTTGTGGCTGCTTTGGACCCCCGTGCTCCTGCAGGGACACTCTGTCTACGGACC
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TGGGACATAGAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCCATGAGGAATTGGTGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 2175)
1 (bases 1 to 2175)
1 (bases 3., Kitagawa, M., Nakayama, K., Shirane, M., Matsumoto, M.,
Hattori, K., Higashi, H., Nakano, H., Okumura, K., Onoe, K., Good, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ubiquitin-dependent degradation of IkappaBalpha is mediated by ubiquitin ligase Skp1/Cul 1/F-box protein FWD1 Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3859-3863 (1999)
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                                  /Product="ubiquitin ligase FWD1"
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/db_xref="gr:4336327"
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NSCARLCINQETYCLTSTAMKTENCVAKAKLANGTSSMIVPKQRKLSASYEKEKELCV
KYFEQNSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENI
LSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIKPMLQRDFITALPARGLDHIAENI
LSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLICARHISLQRIHCRSETSKGVYCLQV
NKPDDENAPPNSFYRALYFKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQV
NKPDDENAPPNSFYRALYFKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQV
NAGEMLNTLIHHCEAVLHLRFNNGMMYTCSKDRSIAVWDMASPDJTLRKYLVGHRAA
NAGEMLNTLIHHCEAVLHLRFNNGMMYTCSKDRSIAVWDMASPDJTLRKYLVGHRAA
                                                                                                                                                                                                                                                                                   /note="similar to beta-transducin repeat-containing protein TrcP; F-box protein; contains WD40 repeats"
TIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLMAALDPRAPAG
                    VNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDN
                                                                                                                                                                                                                                                                         /codon_start=1
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/db_xref="taxon:10090"
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	Db Qy	901 CAGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGGGATAAAAACACATTG 960 	Qу ДЪ
1933 TTTGAGACTC	Q	### 841 CAGAGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGTTTACAGTATGATGAT 900	Qy Db
	Db	781 AAAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGTGGAAGACATAGTTTA 840 	Qy Db
	Qy Qy	721 AAAAACAAACCTCCTGACGGGAATGCTCCTCCCAACTCTTTTTATAGAGCACTTTATCCT 780 	Оу
	Db Ov	7 661 AGGACAGATTCTCTGTGGAGAGGCCTGGCAGAACGAAGAGGATGGGGACAGTATTTATT	Qy Db
	Db.	7 601 GAATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAGAGAATGGTC 660 	Qy Db
	 dd V	541 GAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCAACTTGTGTGCAAG 600 	Оу
	QV DD	481 CCTATGTTGCAGAGAGTTTCATAACTGCTCTGCCAGCTCGGGGATTGGATCATATCGCT 540	Qу
	QV Db	421 GAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCGTATCTTAAA 480	ДУ
	Ov Db	361 AAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTGGAATTTGTG 420 	Фр
	Db Ov	301 GGCACTTCCAGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTATGAAAAGGAA 360 	Qу
	Db Qy	241 TGTTTAGCAAGCACTGCTATGAAGACTGAGAATTGTGTGGCCAAAACAAAACTTGCCAAT 300 	Ωy
	Db Qy	181 AATTCACTTAGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGTA 240 	Qy Db
	ov Ov	121 TCCTCAGAGAGAGAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATACCAGAGAAG 180 	Фр
	Qy Db	61 TCGGCGATTATGGACCCGGCCGAGGCGGTGCTGCAAGAGAGAG	Qу
	Ov Db 1	1 TGCGTTGGCTGCGGCCTGGCACCAAAGGGGGGGGCCCCGGCGGAGAGCGGACCCAGTGGCC 60	Qy Db
1042 AGGGTGATCA	0 da	Query Match 78.2%; Score 1682.2; DB 10; Length 2175; Best Local Similarity 88.5%; Pred. No. 0; Matches 1909; Conservative 0; Mismatches 228; Indels 20; Gaps 7;	Qu Be Ma
	Db Qy	TICLRTLYEHSGRYFRLQFDEFQIYSSSHDDTILIWDFLNDPAAHAEPPRSPSRTYTY BASE COUNT 589 a 528 c 567 g 491 t ORIGIN	BASE ORIG

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                                                                                                                                 TTCCAGAATTCCTCAGAGAGAGAAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATA 210
                                                                                CCAGAGAAGAATTCACTTAGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAA 231
                                                                                                                                                    TTTATGAATTCCTCAGAGAGAGAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATA 171
          Yaron, A., Hatzubai, A., Davis, M., Lavon, I., Amit, S., Mandersen, J.S., Mann, M., Mercurio, F. and Ben-Neriah, Y. Identification of the receptor component of the IkappaBalpha-ubiquitin ligase
Nature 396 (6711), 590-594 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1818 bp mRNA line Homo sapiens b-TRCP variant E3RS-IkappaB mRNA, AF101784.1 GI:4165135
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TGALTAFQNSSERDCNNGEPPRRIIPEKNSLRQTYNSCARLCLUQETVCLLASTAMKT
ENCVAKTKLANGTSSMTLYPKQRKLSASYEKEKELCVKFEQMSESDQVEFVEHLISQL
CHYQHGHINSYLKPMLQRDFITALPARGLDHLAENILSYLDAKSLCAAELVCKEWYRV
TSDGMLMKKLIERWVRTDSLWRGLAERRGWGOYLFKNKPPDCAAPPNSFYRALYPKII
QDLETIESMCRCGRHSLGNHCHAESTEKGVYCLQYDDGKIVSGLRDNTIKIMDKNTLE
CKRILTGHTGSVLCLQYDERVIITGSSDSTVRYWDVNTGEMLNYLIHGEAVLHLRFN
NGMWYGSKORSLAVMDMASFTDITLRRVLVCHRAAVNVDFDDKYIVSASGDRTIKV
WNYSSTCEPTLJGGHKGTACLGVYDBLVYVGSSDNTIRLMDIECGACLRVLEGHEEL
VRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTICLRTLVEHSGRVFRLQFDEE
VRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTICLRTLVEHSGRVFRLQFDEE
QIVSSSHDDTILLMDFLADAQAGEPRSPSRTYTYISR"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="b-TRCP variant E3RS-IkappaB"
/protein_id="AAD08702.1"
/db_xref="GI:4165136"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F-box and WD regions"
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receptor component of KappaBa-ubiquitin ligase; contains
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/db_xref="taxon:9606"
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                                                                     GTTGTAGACTTTGATGACAAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTA
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                                                                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cNA Sequencing by: Sequencing Group at the Stanford Human Genome
center, Stanford University School of Medicine, Stanford, CA 94
Web site:
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (28-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                           This
                                                                                                                                           Clone distribution: MGC clone distribution information can be fo
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 8 Row: o Column: 21
                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                          clone was selected for full length sequencing because it
ed the following selection criteria: matched mRNA gi: 6753209
               /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCGATTATGGACCCGGCAGAGGCGGTGCTGCAGGAGAAAGCGCTTAAGTTTATGAATTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTGGAATTTGTGGAA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTAACAAGCACTGCTATGAAGACTGAAAATTGTGTGGCCAAAGCCAAACTTGCCAATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCACTTAGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGTATGT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCAGAGAGAAAAAATAATAATGGCGAACCCCCTAGGAAGATAATACCAGAGAAAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAGAGAGAGAAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATACCAGAGAAGAAT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGCTGTGTCTCAAGTATTTTGAGCAGTGGTCAGAGTCTGATCAAGTGGAATTTGTAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTTCCAGTATGATTGTGCCCCAAGCAACGGAAACTCTCAGCAAGCTATGAAAAGGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCACTTAGACAGACTTACAACAGCTGTGCCAGGCTTTGCATAAACCAAGAGACACTATGT 180
TGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAGAGAATTGGTCAGG 663
                                                                                                                                                                                                                                AACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTTGTGTGCAAGGAA 603
                                                                                                                                                                                                                                                                                     ATGCTGCAGAGGGATTTCATAACTGCACTGCCAGCACGGGGTCTGGACCACATCGCTGAG
                                                                                                                                                                                                                                                                                                                                        ATGTTGCAGAGAGATTTCATAACTGCTCTGCCAGCTCGGGGATTGGATCATATCGCTGAG
                                                                      TGGTACCGCGTGACGTCGGACGGCATGCTGTGGAAAAAGCTCATCGAGAGGATGGTCAGG
                                                                                                                                                                             AACATTCTGTCATACTTGGACGCCAAGTCACTGTGTGCTGCTGAGCTCGTGTGCAAGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DQKIVSGLRDNTIKIWDKSTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDV
NAGEMLNTLIHHCEAVLHLRFNNGMAVTCSKDRSIAVWDWASPTDITLRRVLVCHRAA
VNVVDFDDKYIVSASGRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDN
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KYPEQMSESDQVEFYEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAEN
LSYLDAKSILCAAELIVCKEWYRYTSOMLWKKLIERMVETDSLAWGGLAERGWGQYLFK
NKPPDENAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHGRSETSKGVYCLQYD
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/protein_id="AAH03989.1"
/db_xref="GI:13278340"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIRLMDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLMAALDPRAPAG
TLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDPAAHAEPPRSPSRTYTY
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/translation="MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTY
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One Baylor Plaza, Houston, TX 77030, USA
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/protein_id="AADA1025.1".
/db_xref="G1:5230822"
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KYFEQWSESDQVEFVEHLISQWCHYQHGHINSYLKPMLQRDFTFALPARGLAERGRGQYLFK
KYFEQWSESDQVEFVEHLISQWCHYQHGHINSYLKPMLQRDFTRALPARGLAERGRGQYLFK
NKPPDENAPPNSTYRALYFKIIQDIETIESNWRCGHHSLQRIHCRSETSKGYVCLQV
NKPDDENAPPNSTYRALYFKIIQDIETIESNWRCGHNSLQRIHCRSETSKGYCLQVD
NAGEMLDTLTHHCEAVLHLERENNGMMTCSKORSLAWDMASSFDITLRRVLVGHRAA
NAGEMLDTLTHHCEAVLHLERENNGMMTCSKORSLAWDMASSFDITLRRVLVGHRAA
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TIRLMDIECGACLRVLEGHEELVRCIRFDNKRIVSGRYDGKIKVWDLMAALDPRAPAG
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GI:4008019 beta-TrCP

SOURCE ORGANISM

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KEYWORDS

REFERENCE

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 1712)

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

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CAGAGAGATTTCATAACTGCTCTGCCAGCTCGGGGATTGGATATCGCTGAGAACATT 549
                                                                               ATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCGTATCTTAAACCTATGTTG
                                                                                                                                                               TGTGTCAAGTATTTTGAGCAGTGGTCAGAGTCTGATCAAGTGGAATTTGTAGAACACCTT
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Direct Submission
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Signal-induced ubiquitination of IkappaBalpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="ubiquitinates phosphorylated IkBa" /note="beta-TrCP; F-box protein; IkB-ubiquitin ligase; substrate recognition subunit of SCF complex; similar to
                                                                                                                                                                                                                                                                                                                   /product="beta-transducin repeat containing protein"
/protein_id="AAN04181.1"
/db_xref="G1:4140718"
/translation="MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTY
/translation="MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTY
/REARLCINGETYCLISTAKKTENCVAKAKLANGTSSMIVPKORKLSASYEKEKELCV
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens beta-TrCP and Drosophila melanogaster Slimb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                          TLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDPAAHAEPPRSPSRTYTY
                                                                                                                                                                                                           TIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLMAALDPRAPAG
                                                                                                                                                                                                                                          DQKIVSGLRDNTIKIWDKSTLECKRILTGHTGSVLCLQYGERVIITGSSDSTVRVWDV
NAGEMLNTLIHHCEAVLHLRFNNGMMYTCSKDRSIAVWDMASPTDITLRRVLVGHRAA
                                                                                                                                                                                                                                                                                      KYFEQWSESDQVEFVEHLISOMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENI
LSYLDAKSLCAAELVCKEWIRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
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                                                                                                                                                                                                                            VNYVDEDDKY I VSASGDRT I KVWNTSTCEFVRT LNGHKRG I ACLQYRDRLVVSGSSDN
                                                                                                                                                                                                                                                                          NKPPDENAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYD
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90.2%;
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Pred. No. 0;
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 ACCCTCCGGAGGGTGCTGGTCGGACACCGAGCTGCTGTCAATGTTGTAGACTTTGATGAC 1269
                                                 GTGACCTGCTCCAAAGATCGTTCCATTGCTGTATGGGATATGGCCTCCCCAACTGACATT 1209
                                                                                                  AACACATTGATTCACCACTGTGAAGCCGTTCTGCACCTGCGCTTCAATAATGGCATGATG
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                                                                                                                                                                                                    Spevak, W., Keiper, B.D., Stratowa, C. and Castanon, M.J. Saccharomyces cerevisiae cdcl5 mutants arrested at a anaphase are rescued by Xenopus cDNAs encoding N-ras with beta-transducin repeats
Mol. Cell. Biol. 13 (8), 4953-4966 (1993)
                                                                                                                                                                                                                                                                                   Xenopodinae; Xenopus.

1 (bases 1 to 1671)
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                               Xenopus laevis
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Xenopus laevis (library: S. cerevisiae expression library X.laevis occytes) cDNA to mRNA.
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M98268.1 GI:295542
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                               /gene="beta-TrCP"
48. .1604
                                                                        oocytes"
                                                                                                                  /organism="Xenopus laevis"
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                                                                                                                                                                Location/Qualifiers
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 GTCTGCAATATGATGAGAGAGTAATCATTACTGGCTCTTCAGACTCTACCGTCCGGGTGT
                                                                                                                     GTCTGCAGTACGATGATCAGAAGATAGTAAGTGGACTCAGAGATAACACCATTAAGATCT
                                                                                                                                                                                                                                        ACAGAGCGCTTTACCCCAAAAATTATTCAAGACATAGAGACAATCGAGTCCAACTGGCGCT
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/protein_id="AAA02810.1"
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/translation="MEGFSCSLQPPTASEREDCURDEPPRKIITEKNTLRQTKLANGT
/translation="MEGFSCSLQPPTASEREDCURDEPPRKIITEKNTLRQTKLANGT
SSMITPKQRKLSANYEKEKELCVKYFEQWSECDQVEFVEHLISRACHYQHGHINTUK
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MVRTDSLWRGLAERRGWGQYLFKNKPPDGKTPPNSFYRALYPKIIQDIETIESNWRCG
RHSLQRIHCRSETSKGVYCLQYDDQKIYSGLRDMTIKINVKNTLECKRYLMGHTGSVL
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AVWDMASATDITLRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVMNTSTCEFVEPTLN
GHKRGJACLQYEDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVS
GAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFTDEFQIVSSSHDDTILI

0; Mismatches 262; Indels DB 5; Length 1671; 0, Gaps

343 0;

157 AGACAAAACTTGCCAATGGCACTTCCAGCATGATTGTGCCCAAGCAGCGAAAACTGTCAG 216 284 AAACAAAACTTGCCAATGGCACTTCCAGTATGATTGTGCCCCAAGCAACGGAAACTCTCAG

217 CAAATTACGAGAAGGAAAAAGAGCTATGCGTCAAGTATTTTGAGCAGTGGTCCGAGTGCG 344 CAAGCTATGAAAAGGAAAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAG 403 ATCAAGTGGAATTTGTGGAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACA 463

TAAACTCGTATCTTAAACCTATGTTGCAGAGAGATTTCATAACTGCTCTGCCAGCTCGGG ATCAAGTAGAGTTTGTTGAACACCTGATATCTCGAATGTGCCACTATCAGCATGGACATA 396 523 336

GACTCGATCACATAGCAGAAAATATACTTTCATACCTGGATGCAAAGTCATTGTGTTCTG GATTGGATCATATCGCTGAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTG 456

643

GGGGACAGTATTTATTCAAAAACAAACCTCCTGACGGGAATGCTCCTCCCAACTCTTTTT

763

576 703

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ATAGAGCACTTTATCCTAAAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGAT

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944 GGGATAAAAACACATTGGAATGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCCTCT

GGGATAAGAATACTTTGGAGTGCAAGCGAGTGCTGATGGGTCACACTGGGTCAGTTCTCT 1003 876

GTCTCCAGTATGATGAGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGT 106: 936

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                                                              Submitted (05-OCT-1999) Masaru Katoh, National Cancer Center, Genetics Division; Tsukiji 5-chome, Chuo-ku, Tokyo 104-0045, Japan (E-mail:mkatoh@ncc.go.jp, Tel:81-3-3542-2511(ex.4402),
                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt BTRCP2}; \ {\tt F-box} and WD-repeats protein beta-TRCP2 isoform Homo sapiens fetal lung cDNA to mRNA.
                                                                                                                                      Direct Submission
                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 269 (1), 103-109 (2000) 20160458
                                                                                                                                                                                                                                              Molecular cloning and genomic structure of the betaTRCP2 chromosome 5q35.1
                                                                                                                                                                                                                                                                                                           Koike,J., Sagara,N., Kirikoshi,H., Takagi,A., Miwa,T., Hirai,M. and
                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                Fax:81-3-3541-2685)
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                              898 GATCAGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGGGATAAAAACACA 957
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                                                                                                                                                                                                                                                                                                 TTCAAAAACAAACCTCCTGACGGGAATGCTCCTCCCAACTCTTTTTATAGAGCACTTTAT 777
                                                                                                                                                                                                                                                                                                                                                GTCAGGACAGATTCTCTGTGGAGAGGCCTGGCAGAACGAAGAGGATGGGGACAGTATTTA 717
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                                                                              TTGCAGAGGATTCAGTGCCGCTCTGAAAATAGTAAAAGGTGTCTACTGTTTACAGTACGAT
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Koike,J., Sagara,N., Kirikoshi,H., Takagi,A., Miwa,T., Hirai,M.
                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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358 GAAAAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTGGAATTT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271 AATGGAACATCATCTGTGATCGTCTCCAGAAAGAGGCCATCAGAAGGAAACTATCAAAAA 330
                                                       GTCAGGACAGATTCTCTGTGGAGAGGCCTGGCAGAACGAAGGGATGGGGACAGTATTTA 717
                                                                                                                                                    AAGGAATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAGAGAATG
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                                                                                                                  AAAGAATGGCAGCGAGTGATCTCAGAAGGAATGCTTTGGAAGAAGCTGATTGAACGAATG
                                                                                                                                                                                                                                    GCAGAAAACATTCTTTCGTACCTGGATGCCAGGTCTCTGTGTGCCAGCAGAGCTGGTATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match,M.
Molecular cloning and genomic structure of the betaTRCP2 gene chromosome 5q35.1
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IVSRKRPSEGNYQKEKDICIKYFDQWSBSDQVEFVEHLISRWRYDHGHINSYLKPMI
QRDFITALPEGOGLDHIARUILSYLDARSICABELYCKEWQRYSEYGHGHINSYLKPMI
QRDFITALPEGOGLDHIARUILSYLDARSICABELYCKEWQRY
TDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKIIQDLETIESMWKKLIERWYR
RIQCRSSNSKGYYCLQYDBEKIISGLEDNSIKIWDKTSECLKYLTGHTGSVLCLQYD
ERVIYTGSSDSTYRVMDYNTGEYLMFLIHHNBAVLHLIFESNGLMYTCSKDRSIAVWDM
ASATDITLRRVLYGHRAAVNYVDFDDKYIVSASGDRTIKVWSTSTCEFVRTLKGHKRG
IACLQYRDRLYVSGSSDNTIRLWDIEGGACLRYLSGHEELVRCIRFDMKRIYSGAYDG
KIKVWDLQAALDPRAPASTICLRTLYEHSGRYFRLQFDEFQIISSSHDDTILLWDFLN
VPPSAQNETRSPSRTYTYISR*
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                                                                                                                                                                                                                                                                                                                            TTGCAAGCTGCTCTTGACCCTCGAGCCCCAGCAAGCACATTGTGTTTTGCGCACATTGGTG
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                                                                                                       CATGATGACACTATTTTGGGATTTCTTAAATGTGCCTCCCAGTGCCCAGAATGAG
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                                                                                         GTGGAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCGTATCTT
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                                                                 GTGGAACATCTTATTTCACGAATGTGTCATTATCAGCATGGACATATTAACTCTTACCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (05-OCT-1999) Masaru Katoh, National Cancer Center, Genetics Division; Tsukiji 5-chome, Chuo-ku, Tokyo 104-0045, Japan (E-mail:mkatoh@ncc.go.jp, Tel:81-3-3542-2511(ex.4402), Fax:81-3-3541-2685)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LINUTE: F-DUX and WD-repeats protein beta-TRCP2 isoform Homo sapiens fetal lung cDNA to mRNA.
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/translation="MEPDSVIEDKTIELMCSVPRSLWLGGANLVESMCALSCLOSMPS
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SHDDTILIWDFLNVPDSAQUETRSPSRTYTYISR"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="BTRCP2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="BTRCP2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue_type="fetal lung"
                                                                                                                                                                                                                                                                                                                                                             41.18;
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                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                        Score 883.4; DB 9;
Pred. No. 2.3e-240;
0; Mismatches 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic structure of the betaTRCP2 gene
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                                                                                                                                                                                                                                                                                                                                                                                Length
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		CATGAGGAATTGGTGCGTTGTATT 149 	IGACAACACTATCAGATTATGGGAC 143 	ACACAAACGAGGCATTGCCTGTTTG 137 CACAAGCGGGGCATTGCCTGTCTC 136	GATAGAACTATAAAGGTATGGAAC 1317 	ACACCGAGCTGCTGTCAATGTTGTA 125 	ATTGCTGTATGGGATATGGCCTCC 119 ATTGCTGTGTGGGACATGGCTTCT 118	AGCAGTTCTGCACTTGCGTTTCAAT 1137 	GTCAGAGTGTGGGATGTAAATACA 1077 	TCAGTCCTCTGTCTCCAGTATGAT 1017 TCTGTCCTCTGTCTGCAGTATGAT 1006	ATCAAGATCTGGGATAAAAACACA 957 ATTAAGATATGGGATAAAACCAGC 946	NGGAGTTTACTGTTTACAGTATGAT 897 NGTGTCTACTGTTTACAGTACGAT 886	AATTGGAGATGTGGAAGACATAGT 837 	AACTCTTTTTATAGAGCACTTTA 	CGAAGAGATGGGGACAGTATTTA 717 AGAAGAGGGTGGGATCAGTACCTG 712	TGGAAGAAGCTTATCGAGAGAATG 657 TGGAAGAAGCTGATTGAACGAATG 652	TCTGTGTGCAGCAGAGCTGGTATGT 592

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